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OM protein - protein search, using sw model

Run on: May 4, 2005, 22:04:58 ; Search time 172 Seconds
(without alignments)
1668.466 Million cell updates/sec

Title: US-10-090-215-12

Perfect score: 3858

Sequence: 1 MADSSGPRAGPGEVAPLG.....GVSKSKHIVKLGSGRRRL 742

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3858	100.0	742	4	Aae06683 Human van
2	3829	99.2	831	8	Adi81606 Human van
3	3829	99.2	871	4	Aae01227 Human van
4	3829	99.2	871	4	Aag65787 Human ion
5	3829	99.2	871	5	Aau74935 Amino aci
6	3829	99.2	871	5	Abb79191 Human VR4
7	3829	99.2	871	5	Adg64947 VANILREP4
8	3829	99.2	871	7	Adg32562 Human TRP
9	3829	99.2	871	7	Adl71047 Type II c
10	3829	99.2	871	8	Adi81584 Human van
11	3829	99.2	871	8	Adi81608 Human OTR
12	3829	99.2	871	8	Adi81588 Human van
13	3828	99.2	871	5	Abb98197 Human VR-
14	3828	99.2	871	8	Adi81590 Human van
15	3828	99.2	871	7	Adi81590 Human van
16	3825	99.1	871	5	Abb98198 Human VR-
17	3823	99.1	871	4	Aae06681 Human van
18	3810	98.8	963	3	Aay96479 Human van
19	3810	98.7	963	5	Aay95381 Human cal
20	3809	98.7	871	4	Aag67210 Amino aci
21	3777.5	97.9	1051	7	Adi808373 Novel pro
22	3695	95.8	871	7	Adl71045 Type II c
23	3695	95.8	871	8	Adi81614 Mouse tra
24	3693	95.7	871	8	Adi81596 Rat vanil
25	3689	95.6	871	4	Aab86980 Murine OT

26	3689	95.6	871	8	Adi81610
27	3685	95.5	871	7	ADG32559
28	3681	95.4	871	4	AAG67209
29	3636	94.2	873	8	ADI81594
30	3472	90.0	803	8	ADI81586
31	3470	89.9	811	4	AAE06682
32	3467	89.9	803	4	AAAG63208
33	3389	87.8	803	8	ADI81592
34	3284	85.1	852	8	ADI81566
35	3120	80.9	743	4	AAAG63209
36	2373.5	61.5	602	5	AAU74936
37	2315.5	60.0	1115	4	ASG28242
38	2156.5	55.9	559	5	AAE16773
39	1808	46.9	498	4	AAE04889
40	1604.5	41.6	843	2	AAU06561
41	1601.5	41.5	843	2	AAW99799
42	1580.5	41.0	838	8	ADI81568
43	1579.5	40.9	838	2	AAU06555
44	1579.5	40.9	838	2	AAW99789
45	1579.5	40.9	838	4	AAE01228

ALIGNMENTS

RESULT 1
AAE06683
ID AAE06683 standard; protein; 742 AA.
XX
AC AAE06683;
XX
DT 16-OCT-2001 (first entry)
XX
DE Human vanilloid receptor VR3 isoform, VR3A+B+.

XX Human; vanilloid receptor; VR3; inflammatory condition; analgesic;
KW intractable pain; postherpetic neuralgia; diabetic neuropathy; asthma;
KW postmastectomy pain; complex regional pain syndrome; arthritis;
KW rheumatoid arthritis; osteoarthritis; ulcer; neurodegenerative disease;
KW chronic obstructive pulmonary disease; irritable bowel syndrome;
KW psoriasis; central nervous system disease; CNS; cancer;
KW intestinal tract disorder; VR3A+B+.

XX Homo sapiens.

XX WO200158945-A1.

XX 16-AUG-2001.

XX 01-FEB-2001; 2001WO-US003456.

XX 08-FEB-2000; 2000US-00500123.

XX (ORTH) ORTHO-MCNEIL, PHARM INC.

XX Dublin AE, Huvar A, Glass CA, Erlander MG;

XX WPI; 2001-489969/53.

XX N-PSDB; AAD12793.

XX New human VR3 receptor useful for the treatment of disorders including cancers arthritis and pain.

XX Claim 11; Fig 8; 10app; English.

XX The patent relates to human vanilloid receptor VR3 polynucleotide and polypeptide. Three isoforms of VR3 namely VR3A-B-, VR3A-B- and VR3A-B+ have also been disclosed. The VR3 polypeptide is used to identify its modulators which are useful for the treatment of inflammatory conditions and for use as analgesics for intractable pain associated with postherpetic neuralgia, diabetic neuropathy, postmastectomy pain, complex regional pain syndromes, arthritis (e.g. rheumatoid and osteoarthritis), as well as ulcers, neurodegenerative diseases, asthma, chronic


```
QY 1 MADSEGRPRAGGEVAELPGDESGTGCGEAFPLSSLANLFEGEDGSLSPSPADASRRPAGP 60
Db 1 MADSEGRPRAGGEVAELPGDESGTGCGEAFPLSSLANLFEGEDGSLSPSPADASRRPAGP 60
QY 61 GDGRNLRMKFQGAERKGVNPNIDLLESTLYESSVVGPKKAPMDSLFDYGYRHHSSDN 120
Db 61 GDGRNLRMKFQGAERKGVNPNIDLLESTLYESSVVGPKKAPMDSLFDYGYRHHSSDN 120
QY 121 KRWKRIIEKQPOSPKAPAPQPPILKVFNNRPIFDIVSRGSTADLDGLLPFLTHKKRL 180
Db 121 KRWKRIIEKQPOSPKAPAPQPPILKVFNNRPIFDIVSRGSTADLDGLLPFLTHKKRL 180
QY 181 TDEPREPSTGKTCLPKALLNSGRNTDIPVLDIAERTGNMREFINSPFRDIYRGOT 240
Db 181 TDEPREPSTGKTCLPKALLNSGRNTDIPVLDIAERTGNMREFINSPFRDIYRGOT 240
QY 241 ALHIAIERCKHYVELLVAQGNADVAQARGFRFPQPKDEGGYFYFGEPLSLAACTNQPHI 300
Db 241 ALHIAIERCKHYVELLVAQGNADVAQARGFRFPQPKDEGGYFYFGEPLSLAACTNQPHI 300
QY 301 VNYLTENPHKKADMRQDSRGNTVLHALVAADNTRENTKFTVMYDILLKLCARLPDS 360
Db 301 VNYLTENPHKKADMRQDSRGNTVLHALVAADNTRENTKFTVMYDILLKLCARLPDS 360
QY 361 NLEAVLNNDGLSPLMAAKTKIGIFQHIIRREVTDTRHLSRKFKDWAYGPVYSSLYD 420
Db 361 NLEAVLNNDGLSPLMAAKTKIGIFQHIIRREVTDTRHLSRKFKDWAYGPVYSSLYD 420
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDWKRFAGVSVINVSYL 480
Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDWKRFAGVSVINVSYL 480
QY 481 AMVIFTLTAYQPLEGTPPYRTTVDYLRAGEVITLTFTGVLPPFTNIKDLFMKKCPGV 540
Db 481 AMVIFTLTAYQPLEGTPPYRTTVDYLRAGEVITLTFTGVLPPFTNIKDLFMKKCPGV 540
QY 541 NSLFDIGSFQLLYFYISVLVISAALYLAGIEAYLAVMVFAVLVGMNVALYFTRGLKLTG 600
Db 541 NSLFDIGSFQLLYFYISVLVISAALYLAGIEAYLAVMVFAVLVGMNVALYFTRGLKLTG 600
QY 601 TYSIMIQILFKDLFRFLVLLFMIGVASALVSLNFCANNKVCNEQDTCTVPTPSC 660
Db 601 TYSIMIQILFKDLFRFLVLLFMIGVASALVSLNFCANNKVCNEQDTCTVPTPSC 660
QY 661 RDSFTSFLLDLRLKLTIGMGDLEMLSTKYPVWFIIILVTVIIITFVLLNMLIALMGE 720
Db 661 RDSFTSFLLDLRLKLTIGMGDLEMLSTKYPVWFIIILVTVIIITFVLLNMLIALMGE 720
QY 721 TVGVSKESKHIWKLIQ 736
Db 721 TVGVSKESKHIWKLIQ 736
```

RESULT 3

AAE01227 standard; protein; 871 AA.

AC AAE01227;
XX
XX 31-JUL-2001 (first entry)
DT
DE Human vanilloid receptor 3 (hVR3) protein.

XX Human; vanilloid receptor 3; VR3; inflammation; arthritis; psoriasis;
KW wound healing; analgesic; vulnerary; antiallergic; gene therapy;
KW neuropathic pain; rhinitis; pruritus; bladder dysfunction;
KW cluster headache; capsaicin-sensitive ion channel disorder.

OS Homo sapiens.

XX FH Key Location/Qualifiers
FT Domain 238..269
FT /label= Ankaryn_repeat

```
FT Domain 284..316  
FT /label= Ankaryn_repeat  
FT Domain 369..402  
FT /label= Ankaryn_repeat  
FT Domain 470..491  
FT /label= Transmembrane_domain  
FT Domain 515..535  
FT /label= Transmembrane_domain  
FT Domain 551..570  
FT /label= Transmembrane_domain  
FT Domain 575..593  
FT /label= Transmembrane_domain  
FT Domain 617..635  
FT /label= Transmembrane_domain  
FT Region 667..681  
FT /label= Poor_loop_region  
FT Domain 693..720  
FT /label= Transmembrane_domain  
XX WO200134805-A2.  
FN 17-MAY-2001.  
XX  
XX 10-NOV-2000; 2000MO-US031077.  
XX 12-NOV-1999; 99US-00438997.  
XX (ABBO ) ABBOTT LAB.  
XX Masters JN, Vos MH;  
XX WPI; 2001-335930/35.  
XX N-PSDB; AAD05107.  
XX Novel human vanilloid receptor gene and encoded polypeptides for  
XX identifying compounds that modulate vanilloid receptors in human tissues  
XX and for treating inflammation, arthritis, psoriasis and wound healing.  
XX Claim 18; Fig 8; 91pp; English.  
XX  
XX The present sequence is human vanilloid receptor 3 (hVR3) protein.  
XX Vanilloid receptor protein and its DNA are useful for identifying  
XX compounds which modulate vanilloid receptors in human tissues, which are  
XX useful for treating various disease states, including neuropathic pain,  
XX inflammation, arthritis, rhinitis, pruritus, bladder dysfunction, cluster  
XX headache, wound healing and psoriasis. Vanilloid receptor DNA is useful  
XX as standard or reagent in diagnostic immunoassays, as targets for  
XX pharmaceutical screening assays and also in gene therapy. Vanilloid  
XX receptor protein is useful for detecting the presence of anti-vanilloid  
XX receptor derived polypeptide in test samples. Vanilloid receptor  
XX antibodies are useful for detecting vanilloid receptor polypeptides, for  
XX screening for diseases or conditions associated with abnormal vanilloid  
XX receptor production, treating disorders involving capsaicin-sensitive ion  
XX channels and as diagnostic markers  
SQ Sequence 871 AA;
```

Query Match 99.2%; Score 3829; DB 4; Length 871;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MADSEGRPRAGGEVAELPGDESGTGCGEAFPLSSLANLFEGEDGSLSPSPADASRRPAGP 60
Db 1 MADSEGRPRAGGEVAELPGDESGTGCGEAFPLSSLANLFEGEDGSLSPSPADASRRPAGP 60
QY 61 GDGRNLRMKFQGAERKGVNPNIDLLESTLYESSVVGPKKAPMDSLFDYGYRHHSSDN 120
Db 61 GDGRNLRMKFQGAERKGVNPNIDLLESTLYESSVVGPKKAPMDSLFDYGYRHHSSDN 120
QY 121 KRWKRIIEKQPOSPKAPAPQPPILKVFNNRPIFDIVSRGSTADLDGLLPFLTHKKRL 180
Db 121 KRWKRIIEKQPOSPKAPAPQPPILKVFNNRPIFDIVSRGSTADLDGLLPFLTHKKRL 180

QY 181 TDEEFREPTGKTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSPPRDIYRGOT 240
 DB |||||
 QY 181 TDEEFREPTGKTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSPPRDIYRGOT 240
 DB |||||
 QY 241 ALHIAIERCKHYVELLVAQAGADVHAQARGFFQPKDEGGYFYGELPLSLAACTNQPHI 300
 DB |||||
 QY 241 ALHIAIERCKHYVELLVAQAGADVHAQARGFFQPKDEGGYFYGELPLSLAACTNQPHI 300
 DB |||||
 QY 301 VNYLTENPHKADMRQDSRGNTVLHALVAIDNTRENTKFTKMDYDGLLLKCARLPDPS 360
 DB |||||
 QY 301 VNYLTENPHKADMRQDSRGNTVLHALVAIDNTRENTKFTKMDYDGLLLKCARLPDPS 360
 DB |||||
 QY 361 NLEAVLNNDGLSPLMMAKTGKIGIFQHIIRREVTDTRHLSRKFKDWAYGVPVSSLYD 420
 DB |||||
 QY 361 NLEAVLNNDGLSPLMMAKTGKIGIFQHIIRREVTDTRHLSRKFKDWAYGVPVSSLYD 420
 DB |||||
 QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWKFKGAVSFYINVSYL 480
 DB |||||
 QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWKFKGAVSFYINVSYL 480
 DB |||||
 QY 481 AMWIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLFTGVLPFTTNKDLFMKKCPGV 540
 DB |||||
 QY 481 AMWIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLFTGVLPFTTNKDLFMKKCPGV 540
 DB |||||
 QY 541 NSLFDGSGFQLLYFYISVLIVSAALYLAGIAYLAVMVFALVGMNVALYFTRGLKLTG 600
 DB |||||
 QY 541 NSLFDGSGFQLLYFYISVLIVSAALYLAGIAYLAVMVFALVGMNVALYFTRGLKLTG 600
 DB |||||
 QY 601 TYSIMIQILFKDLFRLLVYLLFMIGYASALVSLNPNCAVMKVCNEDQTNCTVPTPESC 660
 DB |||||
 QY 601 TYSIMIQILFKDLFRLLVYLLFMIGYASALVSLNPNCAVMKVCNEDQTNCTVPTPESC 660
 DB |||||
 QY 661 RDETFSTFLDLFKLTGMDLEMLSTKYPVVFIIILVYIILTFVLLNMLIALMGE 720
 DB |||||
 QY 661 RDETFSTFLDLFKLTGMDLEMLSTKYPVVFIIILVYIILTFVLLNMLIALMGE 720
 DB |||||
 QY 721 TVGVSKESKHIWKLO 736
 DB |||||
 QY 721 TVGVSKESKHIWKLO 736
 DB |||||

RESULT 4

AAAG65787
 ID AAG65787 standard; protein; 871 AA.

XX AAG65787;

AC AAG65787;

DT 30-JAN-2002 (first entry)

XX Human ion channel VR-5 protein sequence.

DE Ion channel; vanilloid receptor; VR-3; VR-5; nootropic; neuroprotective;

XX antiparkinsonian; analgesic; antidiabetic; antiproliferative; cytostatic;

KW antirheumatic; antiarthritic; gene therapy; antisense therapy.

XX Homo sapiens.

XX WO200168857-A2.

XX 20-SEP-2001.

XX 15-MAR-2001; 2001WO-US008329.

XX 15-MAR-2000; 2000US-00525420.

XX (MILL-) MILLENNIUM PHARM INC.

XX Curtis RAJ, Cook WJ;

XX WPI; 2001-596911/67.

XX N-PSDB; AAI66972, AAI66973.

XX Nucleic acid encoding human ion channels referred to as Vanilloid

PT receptor 3 (VR-3) and VR-5, useful for screening modulators of VR-3 or VR
 PT -5 and for treating calcium homeostasis related disorders (e.g. dementia)
 XX and pain disorders.

XX Claim 13; Fig 2A-C; 167pp; English.

XX The invention provides nucleic acid encoding human ion channels referred
 CC to as vanilloid receptor 3 (VR-3) and VR-5. The VR-3 or VR-5 proteins can
 CC be used to screen for naturally occurring VR-3 or VR-5 ligands or for
 CC drugs or compound which modulate VR-3 or VR-5 activity. The VR-3 or VR-5
 CC proteins and their modulators (e.g. antisense nucleic acids and anti-VR-
 CC antibodies) are useful for treating disorders characterized by
 CC insufficient or excessive production of VR-3 or VR-5. These disorders are
 CC calcium homeostasis related disorders (Alzheimer's disease, dementia,
 CC Parkinson's disease), pain disorders (diabetic neuropathy, rheumatoid
 CC arthritis) and/or cellular growth and/or proliferation disorders (e.g.
 CC cancer). Numerous other examples of these disorders are given in the
 CC specification. The present sequence represents the human VR-5

XX Sequence 871 AA;

XX Query Match 99.2%; Score 3829; DB 4; Length 871;
 XX Best Local Similarity 100.0%; Pred. No. 0;
 XX Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSGPACPGVAVELPGDESGTTCGEAPPLSSLANLFEDEGSLSPSADASRPAGP 60
 DB |||||
 QY 1 MADSSGPACPGVAVELPGDESGTTCGEAPPLSSLANLFEDEGSLSPSADASRPAGP 60
 DB |||||
 QY 61 GDGRPNLRMKFQAGFRKGVNPIDLLLESTLYESSVWPGPKAPMDSLFDTGYTRHSSDN 120
 DB |||||
 QY 61 GDGRPNLRMKFQAGFRKGVNPIDLLLESTLYESSVWPGPKAPMDSLFDTGYTRHSSDN 120
 DB |||||
 QY 121 KRWRKKIIEKQPSKAPAPQPPPIIKVFNRPILFDIVSRGSTADLGLLFLTHKKRL 180
 DB |||||
 QY 121 KRWRKKIIEKQPSKAPAPQPPPIIKVFNRPILFDIVSRGSTADLGLLFLTHKKRL 180
 DB |||||
 QY 181 TDEEFREPTGKTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSPPRDIYRGOT 240
 DB |||||
 QY 181 TDEEFREPTGKTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSPPRDIYRGOT 240
 DB |||||
 QY 241 ALHIAIERCKHYVELLVAQAGADVHAQARGFFQPKDEGGYFYGELPLSLAACTNQPHI 300
 DB |||||
 QY 241 ALHIAIERCKHYVELLVAQAGADVHAQARGFFQPKDEGGYFYGELPLSLAACTNQPHI 300
 DB |||||
 QY 301 VNYLTENPHKADMRQDSRGNTVLHALVAIDNTRENTKFTKMDYDGLLLKCARLPDPS 360
 DB |||||
 QY 301 VNYLTENPHKADMRQDSRGNTVLHALVAIDNTRENTKFTKMDYDGLLLKCARLPDPS 360
 DB |||||
 QY 361 NLEAVLNNDGLSPLMMAKTGKIGIFQHIIRREVTDTRHLSRKFKDWAYGVPVSSLYD 420
 DB |||||
 QY 361 NLEAVLNNDGLSPLMMAKTGKIGIFQHIIRREVTDTRHLSRKFKDWAYGVPVSSLYD 420
 DB |||||
 QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWKFKGAVSFYINVSYL 480
 DB |||||
 QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWKFKGAVSFYINVSYL 480
 DB |||||
 QY 481 AMWIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLFTGVLPFTTNKDLFMKKCPGV 540
 DB |||||
 QY 481 AMWIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLFTGVLPFTTNKDLFMKKCPGV 540
 DB |||||
 QY 541 NSLFDGSGFQLLYFYISVLIVSAALYLAGIAYLAVMVFALVGMNVALYFTRGLKLTG 600
 DB |||||
 QY 541 NSLFDGSGFQLLYFYISVLIVSAALYLAGIAYLAVMVFALVGMNVALYFTRGLKLTG 600
 DB |||||
 QY 601 TYSIMIQILFKDLFRLLVYLLFMIGYASALVSLNPNCAVMKVCNEDQTNCTVPTPESC 660
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 QY 601 TYSIMIQILFKDLFRLLVYLLFMIGYASALVSLNPNCAVMKVCNEDQTNCTVPTPESC 660
 DB |||||
 QY 661 RDETFSTFLDLFKLTGMDLEMLSTKYPVVFIIILVYIILTFVLLNMLIALMGE 720
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 QY 661 RDETFSTFLDLFKLTGMDLEMLSTKYPVVFIIILVYIILTFVLLNMLIALMGE 720
 DB |||||

QY 721 TVGQVSKESKHIWKLIQ 736
DB 721 TVGQVSKESKHIWKLIQ 736

RESULT 5
AAU74935 ID AAU74935 standard; protein; 871 AA.
AC AAU74935;
XX
DT 23-APR-2002 (first entry)
XX
XX Amino acid sequence of human vanilloid receptor-like protein 2a (VRL-2a).
DE Human; vanilloid receptor-like protein 2a; VRL-2a; hypertension;
KW ion-channel protein; pain; osteoarthritis; diabetic neuropathy;
KW neuralgia; nerve injury; neurodegeneration; stroke; inflammation; asthma;
KW allergy; urogenital disorder; incontinence; hypotension;
KW perivascular disease; VRL-related disease; receptor.
XX
OS Homo sapiens.
XX
XX EP1160254-A1.
XX
XX 05-DEC-2001.
XX
XX 25-MAY-2001; 2001EP-00304663.
XX
XX 31-MAY-2000; 2000US-0208156P.
XX
XX (PFIZ) PFIZER INC.
XX
XX Shinjo K, Yabuuchi H;
XX
XX WPI; 2002-084359/12.
XX
XX N-PSDB; ABK14002.
XX
XX New human vanilloid receptor-like proteins, useful for identifying
XX modulators for e.g. treating pain, also related nucleic acid.
XX
XX Claim 1; Page 17-18; 32pp; English.
XX
XX The present invention relates to a new polypeptide that has a sequence
XX 871 amino acids (AAU74935) or 602 amino acids (AAU74936) long, or their
XX variants, as defined in the specification. The polypeptide of the
XX invention is deduced from a human nucleic acid 2749 base pairs (ABK14002)
XX or 1900 base pairs (ABK14003) long, or their variants, also defined in
XX the specification. The polypeptides of the invention, which are human
XX vanilloid receptor-like (VRL) proteins, are used to identify specific
XX modulators that are potentially useful for treating pain (of any origin),
XX osteoarthritis, (diabetic) neuropathy, neuralgia, nerve injury,
XX neurodegeneration, stroke, inflammation, asthma, allergy, urogenital
XX disorders, incontinence, hypo- or hyper-tension and perivascular disease.
XX The molecules of the invention can also be used to raise specific
XX antibodies. The nucleic acid that encodes the polypeptide of the
XX invention is useful for recombinant production of the protein and for
XX preparing transgenic animal models. The polypeptide, antibody and nucleic
XX acid of the invention are also useful as diagnostic agents for
XX determining (susceptibility to) VRL-related diseases. The present amino
XX acid sequence represents the human vanilloid receptor-like protein 2a
XX (VRL-2a) of the invention
XX
XX Sequence 871 AA;

Query Match 99.2%; Score 3829; DB 5; Length 871;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSEGPAGGEVAELPGDESGTFCGAEAPLSSIANLFEGEDGSLSPADASRRPAGP 60
DB 1 MADSSEGPAGGEVAELPGDESGTFCGAEAPLSSIANLFEGEDGSLSPADASRRPAGP 60

QY 61 GDGRPNLMKFGQAFRKGVPNPIDILLESITYESSVVPQKAPMDSLFYGYRHHSSDN 120
DB 61 GDGRPNLMKFGQAFRKGVPNPIDILLESITYESSVVPQKAPMDSLFYGYRHHSSDN 120

QY 121 KRWKKIIEKOQSPKAPAPPPILKVFNPILFDIVSRGSTADLDGLLPFLTHKKEL 180
DB 121 KRWKKIIEKOQSPKAPAPPPILKVFNPILFDIVSRGSTADLDGLLPFLTHKKEL 180

QY 181 TDEEFREPSTGKTCPLPKALLNSGRNDTI PVLLDIAERTGNMREFINSPFEDIYRGQT 240
DB 181 TDEEFREPSTGKTCPLPKALLNSGRNDTI PVLLDIAERTGNMREFINSPFEDIYRGQT 240

QY 241 ALHIAIERRCHYVELLVLAQADVHAQARGFPQKDEGGYFYGELPLSLAACTNQPHI 300
DB 241 ALHIAIERRCHYVELLVLAQADVHAQARGFPQKDEGGYFYGELPLSLAACTNQPHI 300

QY 301 VNYLTENPHKADMRQDSRGNTVLHALVAADNTRENTKFTVMYDILLKLCARLFPDS 360
DB 301 VNYLTENPHKADMRQDSRGNTVLHALVAADNTRENTKFTVMYDILLKLCARLFPDS 360

QY 361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHI IRREVTDETRHLSRKFKDWAYGPVYSSLYD 420
DB 361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHI IRREVTDETRHLSRKFKDWAYGPVYSSLYD 420

QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFIVVSYLC 480
DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFIVVSYLC 480

QY 481 AMVIFTLTAYYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFEEFTNIKDLFMKKCPGV 540
DB 481 AMVIFTLTAYYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFEEFTNIKDLFMKKCPGV 540

QY 541 NSLFIDGSFQLLYFYISVIVSAALYLAGIEAYLAVMVFAVLVGMNVALYFTRGLKLTG 600
DB 541 NSLFIDGSFQLLYFYISVIVSAALYLAGIEAYLAVMVFAVLVGMNVALYFTRGLKLTG 600

QY 601 TYSIMIQKILFKDLFRLLVYLLFMIGYASALVSLNPNCANMKVCNEDQTNCTVPTPSC 660
DB 601 TYSIMIQKILFKDLFRLLVYLLFMIGYASALVSLNPNCANMKVCNEDQTNCTVPTPSC 660

QY 661 RDSFTSFLLDLFKLTIGMGDLEMLSTKYPVVFIIILLVYIILTFVLLNMLALMGE 720
DB 661 RDSFTSFLLDLFKLTIGMGDLEMLSTKYPVVFIIILLVYIILTFVLLNMLALMGE 720

QY 721 TVGQVSKESKHIWKLIQ 736
DB 721 TVGQVSKESKHIWKLIQ 736

RESULT 6
ABB79191 ID ABB79191 standard; protein; 871 AA.
XX
XX AC ABB79191;
XX
XX DT 07-AUG-2002 (first entry)
XX
XX DE Human VR4 protein SEQ ID NO:2.
XX
XX XX Human; VR4; vanilloid 4 receptor; receptor; osteopathic; antirheumatic;
KW antiarthritic; vulnary; analgesic; gene therapy; cartilage; bone;
KW larynx; auditory canal; intravertebral disc; ligament; tendon;
KW joint capsule; bone development disorder; osteoporosis; osteoarthritis;
KW joint destruction; rheumatoid arthritis.
XX
XX OS Homo sapiens.
XX
XX PN WO200234280-A2.
XX
XX PD 02-MAY-2002.
XX
XX PF 25-OCT-2001; 2001WO-GB004739.
XX

PR 25-OCT-2000; 2000GB-00026114.
 XX (SMK) SMITHKLINE BEECHAM PLC.
 PA Davis JB, Gunthorpe MJ, Egerton J, Smart D;
 XX WPI: 2002-471426/50.
 DR N-PSDB; AEN87645.
 XX
 PT Use of vanilloid 4 receptor polypeptide/polynucleotide, a modulator of
 PT the polypeptide or an antisense polynucleotide to the polynucleotide, for
 PT manufacture of a medicament for treating cartilage and/or bone diseases.
 XX
 PS Claim 8; Page 22; 30pp; English.
 XX
 CC The present sequence represents human vanilloid 4 receptor (VR4). VR4 has
 CC osteopathic, antirheumatic, antiarthritic, vulnerary and analgesic
 CC activities. VR4 proteins and polynucleotide sequences can be used in
 CC modulating VR4 activity, in gene therapy and in antisense gene therapy.
 CC VR4 is useful for the manufacture of a medicament for treating diseases
 CC of cartilage and/or bone, or for the treatment of pain associated with
 CC it, where the disease is one affecting the larynx, auditory canal,
 CC intravertebral discs, ligaments, tendons and joint capsules, or a disease
 CC associated with bone development including osteoporosis, or diseases
 CC involving joint destruction such as rheumatoid arthritis or
 CC osteoarthritis, and the pain is associated with rheumatoid arthritis or
 CC osteoarthritis
 XX
 SQ Sequence 871 AA;

Query Match 99.2%; Score 3829; DB 5; Length 871;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSEGPAGCEVAELPGDESGTPGGEAPFLSSLANLFEDEGSLSPADASRRPAGP 60
 Db |||||
 QY 1 MADSEGPAGCEVAELPGDESGTPGGEAPFLSSLANLFEDEGSLSPADASRRPAGP 60
 Db |||||
 QY 61 GDGRNLRMKQAFKRGVNPIDILLESSTLYESSVPGPKAPMDSLFYGYTHHSSDN 120
 Db |||||
 QY 61 GDGRNLRMKQAFKRGVNPIDILLESSTLYESSVPGPKAPMDSLFYGYTHHSSDN 120
 Db |||||
 QY 121 KWRKKIIEKQSPKAPAPPPPIKLVFNRPILFDIVSRGSTDLDGLLPFLTHKKRL 180
 Db |||||
 QY 121 KWRKKIIEKQSPKAPAPPPPIKLVFNRPILFDIVSRGSTDLDGLLPFLTHKKRL 180
 Db |||||
 QY 181 TDEFPREPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSPPFDIYRGQT 240
 Db |||||
 QY 181 TDEFPREPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSPPFDIYRGQT 240
 Db |||||
 QY 241 ALHTAIERCKHYVELLVAQADVHAQARGFFQPKDEGGYFYFGEPLSLAACTNQPHI 300
 Db |||||
 QY 241 ALHTAIERCKHYVELLVAQADVHAQARGFFQPKDEGGYFYFGEPLSLAACTNQPHI 300
 Db |||||
 QY 301 VNYLTENPHKKADMRQDSRGNTVLHALVAJADNTRENTKFTKMDLLKCARLPDS 360
 Db |||||
 QY 301 VNYLTENPHKKADMRQDSRGNTVLHALVAJADNTRENTKFTKMDLLKCARLPDS 360
 Db |||||
 QY 361 NLEAVLNNDGLSPLMAAKTKGIGFQHIIRREVTDTRHLSRKFQDWAYGPVYSSLYD 420
 Db |||||
 QY 361 NLEAVLNNDGLSPLMAAKTKGIGFQHIIRREVTDTRHLSRKFQDWAYGPVYSSLYD 420
 Db |||||
 QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYINVSYL 480
 Db |||||
 QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYINVSYL 480
 Db |||||
 QY 481 AMVFTLTAYTQPLEGTPPYRTTVDYLRAGEVITLFTGVLPFFFTNIKDLFMKCKPGV 540
 Db |||||
 QY 481 AMVFTLTAYTQPLEGTPPYRTTVDYLRAGEVITLFTGVLPFFFTNIKDLFMKCKPGV 540
 Db |||||
 QY 541 NSLFDGSQLLYFTYSVLTVSAALYAGIAYLVANVFAVLVGMNVALYFTRLGLKLTG 600
 Db |||||
 QY 541 NSLFDGSQLLYFTYSVLTVSAALYAGIAYLVANVFAVLVGMNVALYFTRLGLKLTG 600
 Db |||||

QY 601 TYSIMIQILFKDLFRLLVYLLFMIGYASALVSLNPNCANMKVCNEDQTNCTVPTPSC 660
 Db |||||
 QY 601 TYSIMIQILFKDLFRLLVYLLFMIGYASALVSLNPNCANMKVCNEDQTNCTVPTPSC 660
 Db |||||
 QY 661 RDSEFTFLLDLFKLTIGMGDLEMLSTKYPVVFIIILLVYIILTFVLLNMLIALMGE 720
 Db |||||
 QY 661 RDSEFTFLLDLFKLTIGMGDLEMLSTKYPVVFIIILLVYIILTFVLLNMLIALMGE 720
 Db |||||
 QY 721 TVGQVSKESKHILQ 736
 Db |||||
 QY 721 TVGQVSKESKHILQ 736
 Db |||||

RESULT 7
 ADG64947
 ID ADG64947 standard; protein; 871 AA.
 XX
 AC ADG64947;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE VANILREP4 polypeptide of the invention.
 XX
 KW vanilrep4; VR4; Analgesic; cerebroprotective; antiinflammatory;
 KW antidiabetic; anorectic; vasotropic; uropathic; ischemia;
 KW neurodegeneration; inflammatory disorder; irritable bowel syndrome;
 KW diabetes; obesity.
 XX
 OS Homo sapiens.
 XX
 FN EPI170365-A1.
 XX
 PD 09-JAN-2002.
 XX
 PF 04-JUL-2000; 2000EP-00202352.
 XX
 PR 04-JUL-2000; 2000EP-00202352.
 XX
 PA (SMK) SMITHKLINE BEECHAM PLC.
 PI Smith G, Hayes PD, Smart D, Davis JB, Kelsell RE;
 XX
 DR WPI: 2002-156636/21.
 XX
 DR N-PSDB; ADG64946.
 XX

Polypeptide of ion channel family polypeptides, designated vanilrep4,
 useful as a vaccine for inducing immune response against diseases such as
 neuropathies, algesia, nerve injury, ischemia, stroke, incontinence,
 diabetes, obesity.

Claim 1; SEQ ID NO 2; 29pp; English.

The present invention relates to a polypeptide of ion channel family
 polypeptides, vanilrep4 (VR4). The peptides are useful for treating pain
 (e.g. chronic pain, neuropathic pain, post-operative pain, rheumatoid
 arthritis pain), neuralgia, neuropathies, algesia, nerve injury,
 ischemia, neurodegeneration, stroke, incontinence, inflammatory
 disorders, irritable bowel syndrome, diabetes or obesity. Fragments of
 the protein are useful for producing full-length polypeptides by peptide
 synthesis therefore the variants may also be employed as intermediate for
 producing full-length polypeptide. The proteins are also useful for
 identifying agonists or antagonists of peptide activity and expression.
 The peptide is useful as diagnostic reagents for diagnosing a disease or
 a susceptibility to a disease by detecting mutations in the associated
 gene, and is also useful for chromosome localization studies and tissue
 expression studies. The peptide is useful for producing transgenic
 animals, which include knock-in animals (in which an animal gene is
 replaced by human equivalent within the genome of the animal), useful in
 drug discovery process, for target validation, where the compound is
 specific for human target. Peptides and Ab is useful for confining
 screening methods for detecting the effect of added compounds on the
 production of mRNA in cells. The peptides are useful as vaccines for

CC inducing an immunological response in a mammal. The present sequence
CC represents VANILREP4 polypeptide.

XX
SQ Sequence 871 AA;

Query Match 99.2%; Score 3829; DB 5; Length 871;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSEGPAGGGEVAELPGDESGTPGGEAFPLSSLANLFEDEGSLSPSPADASRPAGP 60
Db 1 MADSEGPAGGGEVAELPGDESGTPGGEAFPLSSLANLFEDEGSLSPSPADASRPAGP 60

QY 61 GDGRPNLRMKFQAFKRGVNPIDLESTLYESSVVGPKKAPMDSLFYGYRHHSSDN 120
Db 61 GDGRPNLRMKFQAFKRGVNPIDLESTLYESSVVGPKKAPMDSLFYGYRHHSSDN 120

QY 121 KWRKKIIEKQPSKAPAPQPPPIKVFNRPIFDIVSRGSTADLDGLLPFLTHKKRL 180
Db 121 KWRKKIIEKQPSKAPAPQPPPIKVFNRPIFDIVSRGSTADLDGLLPFLTHKKRL 180

QY 181 TDEEFREPSTGKTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOT 240
Db 181 TDEEFREPSTGKTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOT 240

QY 241 ALHIAIERRCRKHVYELLVAQADVHAQARGFFQPKDEGGYFYFGELPLSLAACTNQPHI 300
Db 241 ALHIAIERRCRKHVYELLVAQADVHAQARGFFQPKDEGGYFYFGELPLSLAACTNQPHI 300

QY 301 VNYLTENPHKADMRQDSRGNTVLHVAIADNTRENTKFTVQYDLLLLKCARLFPDS 360
Db 301 VNYLTENPHKADMRQDSRGNTVLHVAIADNTRENTKFTVQYDLLLLKCARLFPDS 360

QY 361 NLEAVLNNDGSLPMAAKTKIGIFQHLIREVTDTRHLSRKFKDWAYGVPVSSLYD 420
Db 361 NLEAVLNNDGSLPMAAKTKIGIFQHLIREVTDTRHLSRKFKDWAYGVPVSSLYD 420

QY 421 LSSLDTCGEASVLBIYVNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSILC 480
Db 421 LSSLDTCGEASVLBIYVNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSILC 480

QY 481 AMVIFTLTAYQPLEGTPPYRTTVDYLRLAGEVITLFTGVLPFTTNKDLFMKKCPGV 540
Db 481 AMVIFTLTAYQPLEGTPPYRTTVDYLRLAGEVITLFTGVLPFTTNKDLFMKKCPGV 540

QY 541 NSLFDGSGFOLLTYYSVLIVISAALYLAGIAYLAVMVFAVLGMMNALYFTRGLKLTG 600
Db 541 NSLFDGSGFOLLTYYSVLIVISAALYLAGIAYLAVMVFAVLGMMNALYFTRGLKLTG 600

QY 601 TYSIMQKILFKDLFRLLVYLLFMIGVASALVSLNPNCAKMKVCNEQTNCTVPTPSC 660
Db 601 TYSIMQKILFKDLFRLLVYLLFMIGVASALVSLNPNCAKMKVCNEQTNCTVPTPSC 660

QY 661 RDSFTFTFLDLFKLTIGMDLEMLSTKYPVFIILLVTYIILLVLLNMLIALMGE 720
Db 661 RDSFTFTFLDLFKLTIGMDLEMLSTKYPVFIILLVTYIILLVLLNMLIALMGE 720

QY 721 TVGQVSKESKHIWKLO 736
Db 721 TVGQVSKESKHIWKLO 736

RESULT 8

ADG32562
ID ADG32562 standard; protein; 871 AA.
XX
AC ADG32562;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human TRPV4 protein, member of the vanilloid receptor family.
XX
KW human; vanilloid receptor; VR; pain perception; TRPV3; VR1X; VR4;

KW TRPV7; TRPV4; VR13; OTRPC4; TRPM8; TRPX; trkA+; inflammation;
KW skin disorder; cancer; analgesic; antiinflammatory; dermatological;
KW cytosstatic.

XX Homo sapiens.

XX WO2002101045-A2.

XX 19-DEC-2002.

XX 13-JUN-2002; 2002WO-EP006520.

XX 13-JUN-2001; 2001US-0297835P.

XX 22-JAN-2002; 2002US-0351238P.

XX 29-JAN-2002; 2002US-0352914P.

XX 12-FEB-2002; 2002US-0357161P.

XX 15-MAY-2002; 2002US-0381086P.

XX 16-MAY-2002; 2002US-0381739P.

XX (NOVS) NOVARTIS AG.

XX (IRMI-) IRM LLC.

XX Patapoutian A, Song C, Ganju P, Peier A, McIntyre P, Bevan S;

XX WPI; 2003-156962/15.

XX N-PSDB; ADG32561.

XX New isolated TRPV3, TRPV4 or TRPM8 vanilloid receptor nucleic acid

XX molecule and polypeptides, useful for the diagnosis and treatment of

XX disorders such as pain, inflammation, skin diseases and cancer.

XX Claim 69; SEQ ID NO 17; 197pp; English.

XX This invention relates to novel vanilloid receptor (VR) related nucleic
XX acids and encoded proteins thereof. Specifically, it refers to certain
XX members of the VR family that are involved in pain perception, in
XX particular, TRPV3 (previously known as VR13, VR1X, VR4 & TRPV7), TRPV4
XX (previously known as VR13 & OTRPC4) and TRPM8 (previously known as TRPX).
XX Furthermore, this invention includes trkA+ pain specific genes expressed
XX in the sensory neurons of the dorsal root ganglia. Accordingly, such
XX compositions can be useful for the diagnosis, treatment and prevention of
XX pain, inflammation, skin disorders and cancer, and so exhibit analgesic,
XX antiinflammatory, dermatological and cytosstatic activities. This
XX polypeptide sequence is the human TRPV4 protein of the invention.

XX Sequence 871 AA;

Query Match 99.2%; Score 3829; DB 7; Length 871;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSEGPAGGGEVAELPGDESGTPGGEAFPLSSLANLFEDEGSLSPSPADASRPAGP 60

Db 1 MADSEGPAGGGEVAELPGDESGTPGGEAFPLSSLANLFEDEGSLSPSPADASRPAGP 60

QY 61 GDGRPNLRMKFQAFKRGVNPIDLESTLYESSVVGPKKAPMDSLFYGYRHHSSDN 120

Db 61 GDGRPNLRMKFQAFKRGVNPIDLESTLYESSVVGPKKAPMDSLFYGYRHHSSDN 120

QY 121 KWRKKIIEKQPSKAPAPQPPPIKVFNRPIFDIVSRGSTADLDGLLPFLTHKKRL 180

Db 121 KWRKKIIEKQPSKAPAPQPPPIKVFNRPIFDIVSRGSTADLDGLLPFLTHKKRL 180

QY 181 TDEEFREPSTGKTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOT 240

Db 181 TDEEFREPSTGKTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOT 240

QY 241 ALHIAIERRCRKHVYELLVAQADVHAQARGFFQPKDEGGYFYFGELPLSLAACTNQPHI 300

Db 241 ALHIAIERRCRKHVYELLVAQADVHAQARGFFQPKDEGGYFYFGELPLSLAACTNQPHI 300

QY 301 VNYLTENPHKADMRQDSRGNTVLHVAIADNTRENTKFTVQYDLLLLKCARLFPDS 360

|||||

Db 301 VNYLTENPHKKADMRDQSRGNTVLHALVAJADNTRENTKFTVKMYDILLKLCARLFPDS 360
 Qy 361 NLEAVLNNDGLSPLMAAKTKIGIFQHIIRREVTDTRHLSRKFKDWAYGPPVSSLYD 420
 Db 361 NLEAVLNNDGLSPLMAAKTKIGIFQHIIRREVTDTRHLSRKFKDWAYGPPVSSLYD 420
 Qy 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLIC 480
 Db 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLIC 480
 Qy 481 AMVIFTLTAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
 Db 481 AMVIFTLTAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
 Qy 541 NSLFDGSGFQLLYFYISVIVSAALYLAGIAYLAVNVFALVLGWMNALYFTRGLKLTG 600
 Db 541 NSLFDGSGFQLLYFYISVIVSAALYLAGIAYLAVNVFALVLGWMNALYFTRGLKLTG 600
 Qy 601 TYSIMIQILFKDLFRFLVLLFMIGYASALVSLNFCANMKVCNEDQTNCTVPTPSC 660
 Db 601 TYSIMIQILFKDLFRFLVLLFMIGYASALVSLNFCANMKVCNEDQTNCTVPTPSC 660
 Qy 661 RDSEFTSTFLDLFKLTIGMGDLEMLSTKYPVVFIIILLVTVIILTFVLLNMLIALMGE 720
 Db 661 RDSEFTSTFLDLFKLTIGMGDLEMLSTKYPVVFIIILLVTVIILTFVLLNMLIALMGE 720
 Qy 721 TVGQVSKESKHIWKIQ 736
 Db 721 TVGQVSKESKHIWKIQ 736

RESULT 9

IDL71047
 ADL71047 standard; protein; 871 AA.

XX AC ADL71047;

XX DT 20-MAY-2004 (first entry)

XX DE Type II collagen expression promoting protein, seq id 40.

XX KW Osteopathic; antiinflammatory; antirheumatic; antiarthritic;
 XX KW gene therapy; type II collagen; expression; cartilage disease;
 XX KW osteoarthritis; cartilage defect; rheumatoid arthritis; human.

XX OS Homo sapiens.

XX FN WO2003087375-A1.

XX PD 23-OCT-2003.

XX PF 16-APR-2003; 2003WO-JP004802.

XX PR 16-APR-2002; 2002JP-00113908.

XX PR 19-APR-2002; 2002US-0373594P.

XX PA (ASAH) ASAH KASEI KK.

XX PI Matsuda A, Honda G, Muramatsu S;

XX DR WPI; 2003-845331/78.

XX DR N-PSDB; ADL71046.

XX PT New purified protein that promotes type II collagen expression, useful
 XX PT for preventing and treating a cartilage disease, e.g. osteoarthritis,
 XX PT cartilage defect, or rheumatoid arthritis.

XX PS Claim 1; SEQ ID NO 40; 271pp; English.

XX CC The invention relates to a purified protein (I) that promotes type II
 XX CC collagen expression. Also disclosed is an isolated polynucleotide
 XX CC encoding (I), a recombinant vector comprising the polynucleotide and a
 XX CC gene therapeutic agent comprising the recombinant vector as an active

CC ingredient. The proteins, genes, agents and methods are useful for
 CC preventing and treating a cartilage disease, e.g. osteoarthritis,
 CC cartilage defect, or rheumatoid arthritis. The current sequence
 CC represents a human protein that promotes type II collagen expression.

XX SQ Sequence 871 AA;

Query Match 99.2%; Score 3829; DB 7; Length 871;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADSEGPAGGGEVAELPGDESGTPGGEAPPLASLANLFEDEGSLSPADASRRPAGP 60

Db 1 MADSEGPAGGGEVAELPGDESGTPGGEAPPLASLANLFEDEGSLSPADASRRPAGP 60

Qy 61 GDGRPNLRMKFQGAFRKGVNPNIDLLESTLYESSVVPFGKAPMDSLFDYGTGTYRHSSDN 120

Db 61 GDGRPNLRMKFQGAFRKGVNPNIDLLESTLYESSVVPFGKAPMDSLFDYGTGTYRHSSDN 120

Qy 121 KWRKKIIEKQPSKAPAPQPPILKVFNRPIILFIVSRGSTADLDGLLPLLTHKRL 180

Db 121 KWRKKIIEKQPSKAPAPQPPILKVFNRPIILFIVSRGSTADLDGLLPLLTHKRL 180

Qy 181 TDEFRPSPSTGKTCCLKALLNLSGRNDTIPVLIDIAERTGNMREFINSPFRDIYRGQT 240

Db 181 TDEFRPSPSTGKTCCLKALLNLSGRNDTIPVLIDIAERTGNMREFINSPFRDIYRGQT 240

Qy 241 ALHIAIERRCKHYVELLVQAQADVHAQARGFPQKDEGGYFYFGELPLSLAACTNQPHI 300

Db 241 ALHIAIERRCKHYVELLVQAQADVHAQARGFPQKDEGGYFYFGELPLSLAACTNQPHI 300

Qy 301 VNYLTENPHKKADMRDQSRGNTVLHALVAJADNTRENTKFTVKMYDILLKLCARLFPDS 360

Db 301 VNYLTENPHKKADMRDQSRGNTVLHALVAJADNTRENTKFTVKMYDILLKLCARLFPDS 360

Qy 361 NLEAVLNNDGLSPLMAAKTKIGIFQHIIRREVTDTRHLSRKFKDWAYGPPVSSLYD 420

Db 361 NLEAVLNNDGLSPLMAAKTKIGIFQHIIRREVTDTRHLSRKFKDWAYGPPVSSLYD 420

Qy 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLIC 480

Db 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLIC 480

Qy 481 AMVIFTLTAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540

Db 481 AMVIFTLTAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540

Qy 541 NSLFDGSGFQLLYFYISVIVSAALYLAGIAYLAVNVFALVLGWMNALYFTRGLKLTG 600

Db 541 NSLFDGSGFQLLYFYISVIVSAALYLAGIAYLAVNVFALVLGWMNALYFTRGLKLTG 600

Qy 601 TYSIMIQILFKDLFRFLVLLFMIGYASALVSLNFCANMKVCNEDQTNCTVPTPSC 660

Db 601 TYSIMIQILFKDLFRFLVLLFMIGYASALVSLNFCANMKVCNEDQTNCTVPTPSC 660

Qy 661 RDSEFTSTFLDLFKLTIGMGDLEMLSTKYPVVFIIILLVTVIILTFVLLNMLIALMGE 720

Db 661 RDSEFTSTFLDLFKLTIGMGDLEMLSTKYPVVFIIILLVTVIILTFVLLNMLIALMGE 720

Qy 721 TVGQVSKESKHIWKIQ 736

Db 721 TVGQVSKESKHIWKIQ 736

RESULT 10

ADI81584
 ID ADI81584 standard; protein; 871 AA.

XX AC ADI81584;

XX DT 22-APR-2004 (first entry)

XX DE Human vanilloid receptor-related channel like protein.

XX Human; calcium entry modulator; CD4536; CD5842; intracellular calcium;
 KW neurological disease; inflammatory disease; cancer; Alzheimer's disease;
 KW Parkinson's disease; asthma; rheumatoid arthritis; liver disease;
 KW hepatitis; cirrhosis; kidney disease; glomerulonephritis.
 XX
 OS Homo sapiens.
 XX US2004009537-A1.
 XX PD 15-JAN-2004.
 XX
 XX 13-JAN-2003; 2003US-00342844.
 XX
 XX 11-JAN-2002; 2002US-0347459P.
 XX 02-AUG-2002; 2002US-0401171P.
 XX 20-AUG-2002; 2002US-0405678P.
 XX
 XX (ROOS/) ROOS J.
 XX (STAU/) STAUDERMAN K.
 XX (VELI/) VELICELEBI G.
 XX
 XX Roos J, Stauderman K, Velicelebi G;
 PI WPI; 2004-090465/09.
 XX N-PSDB; ADI81583.
 XX
 XX Identifying an agent that modulates intracellular calcium levels, useful
 PT for treating diseases associated with calcium dysregulation (e.g.
 PT cancer), comprises monitoring the effects of the agent on store-operated
 PT calcium entry.
 XX
 XX Disclosure; SEQ ID NO 54; 55pp; English.
 XX
 XX The invention relates to identifying an agent that modulates
 CC intracellular calcium comprises monitoring the effects of the agent on
 CC store-operated calcium entry comprising contacting one or more test cells
 CC or their portion comprising one or more proteins that is (are) at least
 CC about 35% homologous to the protein encoded by Drosophila gene CG4536 or
 CC CG5842 over at least about 40% of the encoded protein (and that provides
 CC for store-operated calcium entry with a test agent), where the portion of
 CC the cell comprises the proteins, monitoring the effect(s) of the test
 CC compound on store-operated calcium entry and identifying a test agent as
 CC an agent if it has an effect on store-operated calcium entry. Also
 CC included are a method of modulating store-operated calcium entry
 CC (comprising modulating the level of, expression of, activity of or
 CC molecular interactions of a protein in a cell that has altered store-
 CC operated calcium entry, where the protein is at least about 35%
 CC homologous to the protein encoded by Drosophila gene CG4536 or CG5842
 CC over at least about 40% of the encoded protein and that provides for
 CC store-operated calcium entry, and where store-operated calcium transport
 CC into the cell is modulated), and a method of identifying a molecule that
 CC provides for store-operated calcium entry (comprising identifying a
 CC molecule that interacts with the protein mentioned above, thus,
 CC identifying molecules involved in modulating store-operated calcium
 CC entry. The protein does not contain the contiguous sequences appearing as
 CC ADI81644 and ADI81645. The proteins are selected from ion transport
 CC proteins. The method is useful in modulating, or in identifying agents
 CC that modulate, intracellular calcium. These may be used in treating
 CC diseases associated with calcium dysregulation, such as neurodegenerative
 CC diseases (e.g. Alzheimer's disease or Parkinson's disease), inflammatory
 CC diseases (e.g. asthma or rheumatoid arthritis), cancer, liver diseases
 CC (e.g. hepatitis or cirrhosis) or kidney diseases (e.g.
 CC glomerulonephritis). The present sequence represents an identified
 CC homologue of one of the two above mentioned drosophila proteins.
 XX
 XX Sequence 871 AA;
 SQ
 Query Match 99.2%; Score 3829; DB 8; Length 871;
 Beat Local Similarity 100.0%; Pred. No. 0;
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MADSEGPAGGVAELPGDESGTGGGAFFLSSLANLFECDGSLSPADASRPGP 60

Db 1 MADSEGPAGGVAELPGDESGTGGGAFFLSSLANLFECDGSLSPADASRPGP 60
 QY 61 GDGRPNLRMKFQGAFRKGVNPIIDLLSTLYESSVPGPKAPMDSLFDYGYRHHSSDN 120
 Db 61 GDGRPNLRMKFQGAFRKGVNPIIDLLSTLYESSVPGPKAPMDSLFDYGYRHHSSDN 120
 QY 121 KRWKRIIEKQSPKAPAPQPPILKVFNRPIILFDIVSRGSTADLDGLLPFLTHKKRL 180
 Db 121 KRWKRIIEKQSPKAPAPQPPILKVFNRPIILFDIVSRGSTADLDGLLPFLTHKKRL 180
 QY 181 TDEFRPSTGKTCIPKALLNSGRNDTIIVLLDIAERTGNMREFFINSPRDIYRGOT 240
 Db 181 TDEFRPSTGKTCIPKALLNSGRNDTIIVLLDIAERTGNMREFFINSPRDIYRGOT 240
 QY 241 ALHIAIERRCKHYVELLVAQADVHAQARGFFQPKDEGGYFYFGELPLSLAACTNQPHI 300
 Db 241 ALHIAIERRCKHYVELLVAQADVHAQARGFFQPKDEGGYFYFGELPLSLAACTNQPHI 300
 QY 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDLLLLKCARLFPS 360
 Db 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDLLLLKCARLFPS 360
 QY 361 NLEAVLNNDGLSPLMAAKTKIGIFQHIIRREVTDTRHLSRKFKDWAYGVPVYSSLYD 420
 Db 361 NLEAVLNNDGLSPLMAAKTKIGIFQHIIRREVTDTRHLSRKFKDWAYGVPVYSSLYD 420
 QY 421 LSSLDTCGEASVLEILLVNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINNVSYLC 480
 Db 421 LSSLDTCGEASVLEILLVNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINNVSYLC 480
 QY 481 AMVIFTLTAYYQPLEGTPPYRTTVDYLRAGEVITLTGVLFFFTNIKOLFMMKKCPGV 540
 Db 481 AMVIFTLTAYYQPLEGTPPYRTTVDYLRAGEVITLTGVLFFFTNIKOLFMMKKCPGV 540
 QY 541 NSLFTDGSFQLLYFYISVLTVSAALYLAGIEAYLVAVFALVGLGMNALYTRGLKLTG 600
 Db 541 NSLFTDGSFQLLYFYISVLTVSAALYLAGIEAYLVAVFALVGLGMNALYTRGLKLTG 600
 QY 601 TYSIMIQILPKDFRLLVLLFMIGVASALVSLNFCANMKVCNEQTNCTVPTYPSC 660
 Db 601 TYSIMIQILPKDFRLLVLLFMIGVASALVSLNFCANMKVCNEQTNCTVPTYPSC 660
 QY 661 RDSEFTSFLLDLFKLTIGMGDLEMLSTKYPVVFILLVTYIILLVLLNMLIALMGE 720
 Db 661 RDSEFTSFLLDLFKLTIGMGDLEMLSTKYPVVFILLVTYIILLVLLNMLIALMGE 720
 QY 721 TVGQVSKESKHIWKIQ 736
 Db 721 TVGQVSKESKHIWKIQ 736
 RESULT 11
 ADI81608
 ID ADI81608 standard; protein; 871 AA.
 XX
 AC ADI81608;
 XX
 DT 22-APR-2004 (first entry)
 DE Human OTRPC4 cation channel.
 XX
 KW Human; calcium entry modulator; CD4536; CD5842; intracellular calcium;
 KW neurological disease; inflammatory disease; cancer; Alzheimer's disease;
 KW Parkinson's disease; asthma; rheumatoid arthritis; liver disease;
 KW hepatitis; cirrhosis; kidney disease; glomerulonephritis.
 XX
 OS Homo sapiens.
 XX US2004009537-A1.
 XX PD 15-JAN-2004.
 XX

PF 13-JAN-2003; 2003US-00342844.
 XX 11-JAN-2002; 2002US-0347459P.
 PR 02-AUG-2002; 2002US-0401171P.
 PR 20-AUG-2002; 2002US-0405678P.
 XX (ROOS/) ROOS J.
 PA (STAU/) STAUDERMAN K.
 PA (VELI/) VELICELEBI G.
 XX
 PI Roos J, Stauderman K, Velicelebi G;
 XX
 XX WPI; 2004-090465/09.
 DR N-PSDB; ADI81607.
 XX
 PT Identifying an agent that modulates intracellular calcium levels, useful
 PT for treating diseases associated with calcium dysregulation (e.g.
 PT cancer), comprises monitoring the effects of the agent on store-operated
 PT calcium entry.
 XX
 PS Disclosure; SEQ ID NO 78; 55pp; English.
 XX
 CC The invention relates to identifying an agent that modulates
 CC intracellular calcium comprises monitoring the effects of the agent on
 CC store-operated calcium entry comprising contacting one or more test cells
 CC or their portion comprising one or more proteins that is (are) at least
 CC about 35% homologous to the protein encoded by Drosophila gene CG4536 or
 CC CG5842 over at least about 40% of the encoded protein (and that provides
 CC for store-operated calcium entry with a test agent), where the portion of
 CC the cell comprises the proteins, monitoring the effect(s) of the test
 CC compound on store-operated calcium entry and identifying a test agent as
 CC an agent if it has an effect on store-operated calcium entry. Also
 CC included are a method of modulating store-operated calcium entry
 CC (comprising modulating the level of, expression of, activity of or
 CC molecular interactions of a protein in a cell that has altered store-
 CC operated calcium entry, where the protein is at least about 35%
 CC homologous to the protein encoded by Drosophila gene CG4536 or CG5842
 CC over at least about 40% of the encoded protein and that provides for
 CC store-operated calcium entry, and where store-operated calcium transport
 CC into the cell is modulated) and a method of identifying a molecule that
 CC provides for store-operated calcium entry (comprising identifying a
 CC molecule that interacts with the protein mentioned above, thus,
 CC identifying molecules involved in modulating store-operated calcium
 CC entry. The protein does not contain the contiguous sequences appearing as
 CC ADI81644 and ADI81645. The proteins are selected from ion transport
 CC proteins. The method is useful in modulating, or in identifying agents
 CC that modulate, intracellular calcium. These may be used in treating
 CC diseases associated with calcium dysregulation, such as neurodegenerative
 CC diseases (e.g. Alzheimer's disease or Parkinson's disease), inflammatory
 CC diseases (e.g. asthma or rheumatoid arthritis), cancer, liver diseases
 CC (e.g. hepatitis or cirrhosis) or kidney diseases (e.g.
 CC glomerulonephritis). The present sequence represents an identified
 CC homologue of one of the two above mentioned drosophila proteins.
 XX
 SQ Sequence 871 AA;

Query Match 99.2%; Score 3829; DB 8; Length 871;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MADSEGPAGGVEAELPGDESGTPGCEAPPLSLANLFEEDGSLSPSPADASRPPAG 60
 Db 1 MADSEGPAGGVEAELPGDESGTPGCEAPPLSLANLFEEDGSLSPSPADASRPPAG 60
 Qy 61 GDGPNLMMKQGAFRKGVNPIIDLESTLYESSVPGPKAPMDSLDYCTYRHSSDN 120
 Db 61 GDGPNLMMKQGAFRKGVNPIIDLESTLYESSVPGPKAPMDSLDYCTYRHSSDN 120
 Qy 121 KRWKRIIEKQPGKAPAPPPPLIKVFNRPILFDIVSRGSTADLDGLLPFLTHKKRL 180
 Db 121 KRWKRIIEKQPGKAPAPPPPLIKVFNRPILFDIVSRGSTADLDGLLPFLTHKKRL 180
 Qy 181 TDEFRPESTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQT 240

Db 181 TDEFRPESTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQT 240
 Qy 241 ALHTAIERRCHYVELLVAAQADVAQARGFFQPKDEGGYFYFGEPLSLAACTNQPHI 300
 Db 241 ALHTAIERRCHYVELLVAAQADVAQARGFFQPKDEGGYFYFGEPLSLAACTNQPHI 300
 Qy 301 VNYLTENPHKKADMRQDSRGNTVLHALVAADNTRENTKFTVMYDILLKLCARLPDS 360
 Db 301 VNYLTENPHKKADMRQDSRGNTVLHALVAADNTRENTKFTVMYDILLKLCARLPDS 360
 Qy 361 NLEAVLNNDGSLPLMAAKTKGIGIFQHIIRREVTDETRHLSRKFKDWAYGPPVSSLYD 420
 Db 361 NLEAVLNNDGSLPLMAAKTKGIGIFQHIIRREVTDETRHLSRKFKDWAYGPPVSSLYD 420
 Qy 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYVNVSYLC 480
 Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYVNVSYLC 480
 Qy 481 AMVIFTLTAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLPFFFTNIKDLFMKKCPGV 540
 Db 481 AMVIFTLTAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLPFFFTNIKDLFMKKCPGV 540
 Qy 541 NSLFIDGSFQLLYFYISVIVSAALYLAGIEAYLVAVMVFALVGLGMMNALYFTRGLKLTG 600
 Db 541 NSLFIDGSFQLLYFYISVIVSAALYLAGIEAYLVAVMVFALVGLGMMNALYFTRGLKLTG 600
 Qy 601 TYSIMIQILFKDLFRLLVYLLFMIGYASALVSLNPNCAVMKVCNEDQTNCTVPTYPSC 660
 Db 601 TYSIMIQILFKDLFRLLVYLLFMIGYASALVSLNPNCAVMKVCNEDQTNCTVPTYPSC 660
 Qy 661 RDSFTSFLLDLFKLITGMGDLMLSGTSPVVFIIILVTYIILTFVLLNMLIALMGE 720
 Db 661 RDSFTSFLLDLFKLITGMGDLMLSGTSPVVFIIILVTYIILTFVLLNMLIALMGE 720
 Qy 721 TVGQVSKESHIWKLQ 736
 Db 721 TVGQVSKESHIWKLQ 736
 RESULT 12
 ADI81588
 ID ADI81588 standard; protein; 871 AA.
 XX
 AC ADI81588;
 XX
 DT 22-APR-2004 (first entry)
 XX Human vanilloid receptor-like channel 2.
 DE
 XX
 KW Human; calcium entry modulator; CD4536; intracellular calcium;
 KW neurological disease; inflammatory disease; cancer; Alzheimer's disease;
 KW Parkinson's disease; asthma; rheumatoid arthritis; liver disease;
 KW hepatitis; cirrhosis; kidney disease; glomerulonephritis.
 XX
 OS Homo sapiens.
 XX
 XX US2004009537-A1.
 XX
 PD 15-JAN-2004.
 XX
 PF 13-JAN-2003; 2003US-00342844.
 XX
 PR 11-JAN-2002; 2002US-0347459P.
 PR 02-AUG-2002; 2002US-0401171P.
 PR 20-AUG-2002; 2002US-0405678P.
 XX
 PA (ROOS/) ROOS J.
 PA (STAU/) STAUDERMAN K.
 PA (VELI/) VELICELEBI G.
 XX
 PI Roos J, Stauderman K, Velicelebi G;
 XX

DR WPI: 2004-090465/09.
 DR N-PSDB; ADI81587.
 XX
 PT Identifying an agent that modulates intracellular calcium levels, useful
 PT for treating diseases associated with calcium dysregulation (e.g.
 PT cancer), comprises monitoring the effects of the agent on store-operated
 PT calcium entry.
 XX
 PS Disclosure; SEQ ID NO 58; 55pp; English.
 XX
 CC The invention relates to identifying an agent that modulates
 CC intracellular calcium comprises monitoring the effects of the agent on
 CC store-operated calcium entry comprising contacting one or more test cells
 CC or their portion comprising one or more proteins that is (are) at least
 CC about 35% homologous to the protein encoded by Drosophila gene CG4536 or
 CC CG5842 over at least about 40% of the encoded protein (and that provides
 CC for store-operated calcium entry with a test agent), where the portion of
 CC the cell comprises the proteins, monitoring the effect(s) of the test
 CC compound on store-operated calcium entry and identifying a test agent as
 CC an agent if it has an effect on store-operated calcium entry. Also
 CC included are a method of modulating store-operated calcium entry
 CC (comprising modulating the level of, expression of, activity of or
 CC molecular interactions of a protein in a cell that has altered store-
 CC operated calcium entry, where the protein is at least about 35%
 CC homologous to the protein encoded by Drosophila gene CG4536 or CG5842
 CC over at least about 40% of the encoded protein and that provides for
 CC store-operated calcium entry, and where store-operated calcium transport
 CC into the cell is modulated) and a method of identifying a molecule that
 CC provides for store-operated calcium entry (comprising identifying a
 CC molecule that interacts with the protein mentioned above, thus,
 CC identifying molecules involved in modulating store-operated calcium
 CC entry. The protein does not contain the contiguous sequences appearing as
 CC ADI81644 and ADI81645. The proteins are selected from ion transport
 CC proteins. The method is useful in modulating, or in identifying agents
 CC that modulate, intracellular calcium. These may be used in treating
 CC diseases associated with calcium dysregulation, such as neurodegenerative
 CC diseases (e.g. Alzheimer's disease or Parkinson's disease), inflammatory
 CC diseases (e.g. asthma or rheumatoid arthritis), cancer, liver diseases
 CC (e.g. hepatitis or cirrhosis) or kidney diseases (e.g.
 CC glomerulonephritis). The present sequence represents an identified
 CC homologue of one of the two above mentioned drosophila proteins.
 XX
 SQ Sequence 871 AA;
 Query Match 99.2%; Score 3829; DB 8; Length 871;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MADSEGPAGGGEVAELPGDESGTPGGEAFPLSSLANLFEDEGSLSPSPADASRRPAG 60
 DB 1 MADSEGPAGGGEVAELPGDESGTPGGEAFPLSSLANLFEDEGSLSPSPADASRRPAG 60
 QY 61 GGRNLRMKFGAARPKGVNPDILLESTLYESSVPGPKAPMDSLFYGYRHHSDN 120
 DB 61 GGRNLRMKFGAARPKGVNPDILLESTLYESSVPGPKAPMDSLFYGYRHHSDN 120
 QY 121 KWRKKIIEKQSPKAPAPPPPIKVFNRPIFDIVSRGSTADLDGLPPLLTHKKRL 180
 DB 121 KWRKKIIEKQSPKAPAPPPPIKVFNRPIFDIVSRGSTADLDGLPPLLTHKKRL 180
 QY 181 TDEEFREPTGKTCPLKALLNSGRNDTIPVLLDIAERTGNRRFINSPPFDIYRGQT 240
 DB 181 TDEEFREPTGKTCPLKALLNSGRNDTIPVLLDIAERTGNRRFINSPPFDIYRGQT 240
 QY 241 ALHIAIERCKHYVELLVAQAGADVAQAGRRFPQPKDEGGYFYGELPLSLAACTNQPHI 300
 DB 241 ALHIAIERCKHYVELLVAQAGADVAQAGRRFPQPKDEGGYFYGELPLSLAACTNQPHI 300
 QY 301 VNYLTENPHKADMRQDSRGNTVLHVAIADNTRENTKFTVMYDILLKLCARLFPDS 360
 DB 301 VNYLTENPHKADMRQDSRGNTVLHVAIADNTRENTKFTVMYDILLKLCARLFPDS 360
 QY 361 NLEAVLNNDGLSPLMAAKTGKIGIFQHIIRREVTDTRHLSRKFKDWAYGPVYSSLYD 420

DB 361 NLEAVLNNDGLSPLMAAKTGKIGIFQHIIRREVTDTRHLSRKFKDWAYGPVYSSLYD 420
 QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINNVSYLC 480
 DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINNVSYLC 480
 QY 481 AMVIFTLTAYYQPLEGTPPYRTTVDYLRLAGEVITLFTGVLFVFFFTNIKOLFMMKKCPGV 540
 DB 481 AMVIFTLTAYYQPLEGTPPYRTTVDYLRLAGEVITLFTGVLFVFFFTNIKOLFMMKKCPGV 540
 QY 541 NSLIDGFSQLLYFYISVLTVSAAALYLAGTEAVLAVMVFALVGMNVALYFTRGLKLTG 600
 DB 541 NSLIDGFSQLLYFYISVLTVSAAALYLAGTEAVLAVMVFALVGMNVALYFTRGLKLTG 600
 QY 601 TYSIMIOKILFKDLFRLLVLLFPMIGYASALVSLNPNCAKMKVCNEQTNCTVPTPSC 660
 DB 601 TYSIMIOKILFKDLFRLLVLLFPMIGYASALVSLNPNCAKMKVCNEQTNCTVPTPSC 660
 QY 661 RDSFTSTFLLDLFKLTGMGDLMLSTKYPVVFILLVYIILTVLLNMLIALMGE 720
 DB 661 RDSFTSTFLLDLFKLTGMGDLMLSTKYPVVFILLVYIILTVLLNMLIALMGE 720
 QY 721 TVGQVSKESKHIWKLQ 736
 DB 721 TVGQVSKESKHIWKLQ 736
 RESULT 13
 ABB98197
 ID ABB98197 standard; protein; 871 AA.
 XX
 AC ABB98197;
 DT 12-DEC-2002 (first entry)
 XX
 DE Human VR-OAC amino acid sequence.
 XX
 KW Human; VR-OAC; vanilloid receptor-related osmotically activated channel;
 KW anti-HIV; antiaesthetic; immunomodulator; cerebroprotective;
 KW antidiabetic; antiinfertility; auditory; antipruritic; dermatological;
 KW anipsoratic; antiallergic; anorectic; neuroprotective;
 KW ophthalmological; nootropic; cytotatic; nephrotropic; hypotensive;
 KW analgesic; mechanoreception; mechanosensation; hearing disorder; HIV;
 KW Human immunodeficiency virus; obesity; vertigo; motion sickness;
 KW neurological disorder; ataxia; male infertility; immune dysfunction;
 KW diabetes mellitus; chronic obstructive lung disorder; bronchial asthma;
 KW sexual dysfunction; blindness; skin disorder; psoriasis; kidney disease;
 KW arterial hypertension; pain syndrome; Alzheimer's disease; dementia;
 KW hydrocephalus; alopecia; baldness; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200259152-A2.
 XX
 PD 01-AUG-2002.
 XX
 XX 26-OCT-2001; 2001WO-US050539.
 PF
 XX 26-OCT-2000; 2000US-0243568P.
 PR
 XX 25-OCT-2001; 2001US-00243568.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Liedtke W, Heller S, Hudspeth AJ, Friedman JM;
 XX
 DR WPI: 2002-599762/64.
 DR N-PSDB; ABQ79489.
 XX
 PT Modulating mechanoreception or mechanosensation, for diagnosing,
 PT preventing or treating e.g. hearing disorders, HIV or obesity, comprises
 PT administering a vanilloid receptor-related osmotically activated channel
 PT polypeptide.

XX Claim 2; Fig 2; 154pp; English.

XX The invention relates to modulating mechanoreception/mechanosensation in

XX a mammal by administering a vanilloid receptor-related osmotically

XX activated channel (VR-OAC) polypeptide, its active fragments or portions,

XX or by introducing a nucleic acid vector capable of expressing the VR-OAC

XX polypeptide. The method of the invention is useful for modulating or

XX mechanoreception or mechanosensation, for diagnosing, preventing or

XX treating e.g. hearing disorders, human immunodeficiency virus (HIV),

XX obesity, vertigo of labyrinthine origin including motion sickness,

XX neurological disorders including ataxia, male infertility, immune

XX dysfunction, diabetes mellitus, chronic obstructive lung disorder,

XX bronchial asthma, sexual dysfunction, blindness due to corneal or retinal

XX causes, or skin disorders including psoriasis. Other conditions include

XX arterial hypertension, kidney diseases, pain syndromes, Alzheimer's

XX disease and other dementias, hydrocephalus, alopecia, baldness and

XX cancer. The VR-OAC may be used in detecting or assessing osmotic and

XX mechanical stimuli, or as the facilitating component in translating an

XX osmotic or mechanical stimulus in nano-technological, biosensor or

XX biorobotic devices. The current sequence represents the amino acid

XX sequence of human VR-OAC as determined from HEK293 cells. NOTE: The

XX inventors indicate the presence of further VR-OAC polypeptides other than

XX those given in records ABB98197-8. However, no sequence information

XX regarding these polypeptides which are referred to as SEQ ID's 5, 6, 7, 8

XX and 9 is given

SQ Sequence 871 AA;

Query Match 99.2%; Score 3828; DB 5; Length 871;

Best Local Similarity - 99.9%; Pred. No. 0;

Matches 735; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSEGRAGCEVAELPGDESGTPGCEAPLSSIANLFGEDGSLSPSPADASRPGP 60

DB 1 MADSEGRAGCEVAELPGDESGTPGCEAPLSSIANLFGEDGSLSPSPADASRPGP 60

QY 61 GDGRENLRMKFOGAFKRGVNPIDLLESTLYESSVVPKAPMDSLFDYGYRHHSDN 120

DB 61 GDGRENLRMKFOGAFKRGVNPIDLLESTLYESSVVPKAPMDSLFDYGYRHHSDN 120

QY 121 KWRKKIIEKQPSKAPAPOPPPILKVFNRPIPLFDIVSRGSTDLDGLLPFLTHKRL 180

DB 121 KWRKKIIEKQPSKAPAPOPPPILKVFNRPIPLFDIVSRGSTDLDGLLPFLTHKRL 180

QY 181 TDEEPREPTGKTCPLKALLNSGRNTIPVLLDIAERTGNMREFFINSFRDIYRGOT 240

DB 181 TDEEPREPTGKTCPLKALLNSGRNTIPVLLDIAERTGNMREFFINSFRDIYRGOT 240

QY 241 ALHIAIERCKHYVELLVQAQADVHAQARFFQPKDEGGYFYFGEPLSLAACTNQPHI 300

DB 241 ALHIAIERCKHYVELLVQAQADVHAQARFFQPKDEGGYFYFGEPLSLAACTNQPHI 300

QY 301 VNYLTENPHKKADMRQDSRGNTVLHALVAJADNTRENTKFTVMYDLLLLKCARLPDPS 360

DB 301 VNYLTENPHKKADMRQDSRGNTVLHALVAJADNTRENTKFTVMYDLLLLKCARLPDPS 360

QY 361 NLEAVLNNDGSLPLMAAKTKIGIFQHIIRREVTDTRHLSRKFDKWAYGPIVSSLYD 420

DB 361 NLEAVLNNDGSLPLMAAKTKIGIFQHIIRREVTDTRHLSRKFDKWAYGPIVSSLYD 420

QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYINVSVYLC 480

DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYINVSVYLC 480

QY 481 AMVIFTLTAYQPLEGTPPYRTTVDVLRAGEVITLFTGVLFPPFTNIKOLFMMKCPGV 540

DB 481 AMVIFTLTAYQPLEGTPPYRTTVDVLRAGEVITLFTGVLFPPFTNIKOLFMMKCPGV 540

QY 541 NSLFDGSGFQLLYFTYSVLIVSAAALYLAGIAYLVAVNMVFLVGMNNAVFTRLGLKTG 600

DB 541 NSLFDGSGFQLLYFTYSVLIVSAAALYLAGIAYLVAVNMVFLVGMNNAVFTRLGLKTG 600

QY 601 TYSIMIQKILFKDLFRFLVLLFMIGYASALVSLNPCANNKVCNEDQTNCTVPTPSC 660

DB 601 TYSIMIQKILFKDLFRFLVLLFMIGYASALVSLNPCANNKVCNEDQTNCTVPTPSC 660

QY 661 RDSEFTSFLLDLFLKLTIGMGDLEMLSSTKYPVVFIIILVTYIIILTFVLLNNLIALMGE 720

DB 661 RDSEFTSFLLDLFLKLTIGMGDLEMLSSTKYPVVFIIILVTYIIILTFVLLNNLIALMGE 720

QY 721 TVGQVSKSKHIWKLQ 736

DB 721 TVGQVSKSKHIWKLQ 736

RESULT 14

ID ADI81590 standard; protein; 871 AA.

XX AC ADI81590;

XX DT 22-APR-2004 (first entry)

XX DE Human vanilloid receptor-related channel protein #1.

XX KW Human; calcium entry modulator; CD4536; CD5842; intracellular calcium;

XX KW neurological disease; inflammatory disease; cancer; Alzheimer's disease;

XX KW Parkinson's disease; asthma; rheumatoid arthritis; liver disease;

XX KW hepatitis; cirrhosis; kidney disease; glomerulonephritis.

XX OS Homo sapiens.

XX PN US2004009537-A1.

XX PD 15-JAN-2004.

XX PF 13-JAN-2003; 2003US-00342844.

XX PR 11-JAN-2002; 2002US-0347459P.

XX PR 02-AUG-2002; 2002US-0401171P.

XX PR 20-AUG-2002; 2002US-0405678P.

XX PA (ROOS/) ROOS J.

XX PA (STAU/) STAUDERMAN K.

XX PA (VELI/) VELICELEBI G.

XX PI Roos J, Stauderman K, Velicelebi G;

XX WPI; 2004-090465/09.

XX DR N-PSDB; ADI81589.

XX PT Identifying an agent that modulates intracellular calcium levels, useful

XX for treating diseases associated with calcium dysregulation (e.g.

XX cancer), comprises monitoring the effects of the agent on store-operated

XX calcium entry.

XX PS Disclosure; SEQ ID NO 60; 55pp; English.

XX CC The invention relates to identifying an agent that modulates

XX intracellular calcium comprises monitoring the effects of the agent on

XX store-operated calcium entry comprising contacting one or more test cells

XX or their portion comprising one or more proteins that is (are) at least

XX about 35% homologous to the protein encoded by Drosophila gene CG4536 or

XX CG5842 over at least about 40% of the encoded protein (and that provides

XX for store-operated calcium entry with a test agent), where the portion of

XX the cell comprises the proteins, monitoring the effect(s) of the test

XX compound on store-operated calcium entry and identifying a test agent as

XX an agent if it has an effect on store-operated calcium entry. Also

XX included are a method of modulating store-operated calcium entry

XX (comprising modulating the level of, expression of, activity of or

XX molecular interactions of a protein in a cell that has altered store-

XX operated calcium entry, where the protein is at least about 35%

XX homologous to the protein encoded by Drosophila gene CG4536 or CG5842

XX over at least about 40% of the encoded protein and that provides for

XX store-operated calcium entry, and where store-operated calcium transport

CC into the cell is modulated) and a method of identifying a molecule that
 CC provides for store-operated calcium entry (comprising identifying a
 CC molecule that interacts with the protein mentioned above, thus,
 CC identifying molecules involved in modulating store-operated calcium
 CC entry. The protein does not contain the contiguous sequences appearing as
 CC AD181644 and AD181645. The proteins are selected from ion transport
 CC proteins. The method is useful in modulating, or in identifying agents
 CC that modulate, intracellular calcium. These may be used in treating
 CC diseases associated with calcium dysregulation, such as neurodegenerative
 CC diseases (e.g. Alzheimer's disease or Parkinson's disease), inflammatory
 CC diseases (e.g. asthma or rheumatoid arthritis), cancer, liver diseases
 CC (e.g. hepatitis or cirrhosis) or kidney diseases (e.g.
 CC glomerulonephritis). The present sequence represents an identified
 CC homologue of one of the two above mentioned drosophila proteins.
 XX
 SQ Sequence 871 AA;

Query Match 99.2%; Score 3828; DB 8; Length 871;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 735; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSEGPAGGEVAELPGDESGTPGGEAFPLSSLANLFECEGSLSPADASRPAGP 60
 DB 1 MADSEGPAGGEVAELPGDESGTPGGEAFPLSSLANLFECEGSLSPADASRPAGP 60

QY 61 GDGRNLRMKFCQAFKRGKVPNPIDLLESTLYESSVVPKAPMDSLDYGYRHHSSDN 120
 DB 61 GDGRNLRMKFCQAFKRGKVPNPIDLLESTLYESSVVPKAPMDSLDYGYRHHSSDN 120

QY 121 KWRKKIIEKQPSKAPAPQPPILKVFNRPIFDIVSRGSTADLDGLLPFLTHKKRL 180
 DB 121 KWRKKIIEKQPSKAPAPQPPILKVFNRPIFDIVSRGSTADLDGLLPFLTHKKRL 180

QY 181 TDEEREESTGTCLPKALLNLSNGRNDIPVLDIAERTGNMREFFINSPPDIYRGOT 240
 DB 181 TDEEREESTGTCLPKALLNLSNGRNDIPVLDIAERTGNMREFFINSPPDIYRGOT 240

QY 241 ALHIAIERCKHYVELLVQAQADVAQARGRFQPKDEGGYFYGELPLSLAECTNQPHI 300
 DB 241 ALHIAIERCKHYVELLVQAQADVAQARGRFQPKDEGGYFYGELPLSLAECTNQPHI 300

QY 301 NYLNTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDLLLLKCARLPDS 360
 DB 301 NYLNTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDLLLLKCARLPDS 360

QY 361 NLEAVLNNDGLSPLMAAKTKIGIFQHIIRREVTDETRHLSRKFKDWAYGPNVSSLYD 420
 DB 361 NLEAVLNNDGLSPLMAAKTKIGIFQHIIRREVTDETRHLSRKFKDWAYGPNVSSLYD 420

QY 421 LSSLDTCGEASVLETLVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLC 480
 DB 421 LSSLDTCGEASVLETLVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLC 480

QY 481 AMVIFTLTAYQPLEGTPPYRTTVDYLRLAGEVITLFTGVLFPFTNIKOLFMRKCPGV 540
 DB 481 AMVIFTLTAYQPLEGTPPYRTTVDYLRLAGEVITLFTGVLFPFTNIKOLFMRKCPGV 540

QY 541 NSLFDGSPQLLYFYISVLVYSAALYLAGIAYLAVWVFLVGLWMNALYFTRGKLTG 600
 DB 541 NSLFDGSPQLLYFYISVLVYSAALYLAGIAYLAVWVFLVGLWMNALYFTRGKLTG 600

QY 601 TYSIMIQKLFKDLFRFLVLVLLFMIGYASALVSLNCPANKVCNEDTCTVTPYPS 660
 DB 601 TYSIMIQKLFKDLFRFLVLVLLFMIGYASALVSLNCPANKVCNEDTCTVTPYPS 660

QY 661 RDSFTSTFLDLFKLTIGMGLMELSSSTKYPVVFIIILVTVIILFTVLLANLALMGE 720
 DB 661 RDSFTSTFLDLFKLTIGMGLMELSSSTKYPVVFIIILVTVIILFTVLLANLALMGE 720

QY 721 TVGVQSKESKHIWKQLQ 736
 DB 721 TVGVQSKESKHIWKQLQ 736

RESULT 15
 ADE08372
 ID ADE08372 standard; protein; 970 AA.
 XX
 AC ADE08372;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Novel protein (useful for identifying genetic disorders) #527.
 XX
 KW novel gene; novel protein; tissue marker; molecular weight marker;
 KW chromosome marker; genetic disorder.
 XX
 OS Unidentified.
 XX
 FN WO2003054152-A2.
 XX
 PD 03-JUL-2003.
 XX
 PF 10-DEC-2002; 2002WO-US039555.
 XX
 PR 10-DEC-2001; 2001US-0339739P.
 PR 11-DEC-2001; 2001US-0339453P.
 PR 14-MAR-2002; 2002US-0365091P.
 PR 14-MAR-2002; 2002US-0365384P.
 PR 12-APR-2002; 2002US-0372381P.
 PR 12-APR-2002; 2002US-0372615P.
 PR 22-APR-2002; 2002US-00128558.
 PR 24-APR-2002; 2002US-0376045P.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
 PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
 PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
 XX
 WI WPI; 2003-569235/53.
 DR N-PSDB; ADE07461.
 XX
 PT New polynucleotides, useful for expressing recombinant proteins for
 PT analysis, characterization or therapeutic use, or as markers for tissues
 PT in which the corresponding protein is preferentially expressed.
 XX
 PS Claim 20; SEQ ID NO 1438; 1177pp; English.
 XX
 CC The invention comprises the amino acid and coding sequences of novel
 CC proteins. The DNA and protein sequences of the invention are useful as:
 CC markers for tissues in which the corresponding protein is preferentially
 CC expressed; as molecular weight markers on gels; as chromosome markers or
 CC tags; to identify chromosomes or to map related gene positions; and to
 CC compare with endogenous DNA sequences in patients to identify potential
 CC genetic disorders. The present amino acid sequence represents a protein
 CC of the invention.
 XX
 SQ Sequence 970 AA;

Query Match 99.2%; Score 3828; DB 7; Length 970;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 735; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSEGPAGGEVAELPGDESGTPGGEAFPLSSLANLFECEGSLSPADASRPAGP 60
 DB 100 MADSEGPAGGEVAELPGDESGTPGGEAFPLSSLANLFECEGSLSPADASRPAGP 159

QY 61 GDGRNLRMKFCQAFKRGKVPNPIDLLESTLYESSVVPKAPMDSLDYGYRHHSSDN 120
 DB 160 GDGRNLRMKFCQAFKRGKVPNPIDLLESTLYESSVVPKAPMDSLDYGYRHHSSDN 219

QY 121 KWRKKIIEKQPSKAPAPQPPILKVFNRPIFDIVSRGSTADLDGLLPFLTHKKRL 180
 DB 220 KWRKKIIEKQPSKAPAPQPPILKVFNRPIFDIVSRGSTADLDGLLPFLTHKKRL 279

Qy	181	TDEEFREPSTGTCPLPKALLNLSGRNDTIPVLLDIAERTGNMREFINSPPFDIYYRGOT	240
Db	280	TDEEFREPSTGTCPLPKALLNLSGRNDTIPVLLDIAERTGNMREFINSPPFDIYYRGOT	339
Qy	241	ALHIAIERCKHYVELLVQAQADVHAQARGRFFQPKDEGGYFYGELPLSLAACTNQPHI	300
Db	340	ALHIAIERCKHYVELLVQAQADVHAQARGRFFQPKDEGGYFYGELPLSLAACTNQPHI	399
Qy	301	VNYLTENPHKKADMRRODSRGNTVLHALVAIADNTRENTKFTVMYDLLLLKCARLFPDS	360
Db	400	VNYLTENPHKKADMRRODSRGNTVLHALVAIADNTRENTKFTVMYDLLLLKCARLFPDS	459
Qy	361	NLEAVLNNDGLSPLMAAKTGIGIFQHIIIRREVTDTRHLSRKFKDWAYGVPVYSSLYD	420
Db	460	NLEAVLNNDGLSPLMAAKTGIGIFQHIIIRREVTDTRHLSRKFKDWAYGVPVYSSLYD	519
Qy	421	LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELRDKWRKFGAVSFYINVVSYLE	480
Db	520	LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELRDKWRKFGAVSFYINVVSYLE	579
Qy	481	AMVIFTLTAYYQPLEGTPPYRTTVDYLRAGEVITLTGVLFFFTNFKDLFMKKCPGV	540
Db	580	AMVIFTLTAYYQPLEGTPPYRTTVDYLRAGEVITLTGVLFFFTNFKDLFMKKCPGV	639
Qy	541	NSLFDGSGFQLLYFYISVLIVSAALYLAGIEAYLAVMVFALVGLWMNALYFTRGLKLTG	600
Db	640	NSLFDGSGFQLLYFYISVLIVSAALYLAGIEAYLAVMVFALVGLWMNALYFTRGLKLTG	699
Qy	601	TYSIMIQKILFKDLFRLLVYLLFMIGVASALVSLNPCANNKVCNEDQTNCTVPTPSC	660
Db	700	TYSIMIQKILFKDLFRLLVYLLFMIGVASALVSLNPCANNKVCNEDQTNCTVPTPSC	759
Qy	661	RSETFSTFLDLFKLTICMGDLEMLSSTKYPVVFIIILVTYIILTFVLLNMLIALMGE	720
Db	760	RSETFSTFLDLFKLTICMGDLEMLSSTKYPVVFIIILVTYIILTFVLLNMLIALMGE	819
Qy	721	TVGQVSKEKSHIWKLO 736	
Db	820	TVGQVSKEKSHIWKLO 835	

Search completed: May 4, 2005, 22:15:21
Job time : 177 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rnp**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:
<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher. When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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OM protein - protein search, using sw model

Run on: May 4, 2005, 22:10:59 ; Search time 43 Seconds
(without alignments)
1288.130 Million cell updates/sec

Title: US-10-090-215-12

Perfect score: 3858

Sequence: 1 MADSEGPAGPGEVAELPG.....QGVSKSHIWKLOSGRRRL 742

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS-COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3858	100.0	742	US-09-500-123-12	Sequence 12, Appl
2	3823	99.1	871	US-09-500-123-7	Sequence 7, Appl
3	3470	89.9	811	US-09-500-123-9	Sequence 9, Appl
4	1604.5	41.6	843	US-09-235-451-25	Sequence 25, Appl
5	1604.5	41.6	843	US-09-978-303-25	Sequence 25, Appl
6	1579.5	40.9	838	US-09-235-451-2	Sequence 2, Appl
7	1579.5	40.9	838	US-09-132-316-3	Sequence 3, Appl
8	1579.5	40.9	838	US-09-667-422-9	Sequence 9, Appl
9	1579.5	40.9	838	US-09-978-303-2	Sequence 2, Appl
10	1557.5	40.4	839	US-09-197-636-2	Sequence 2, Appl
11	1556.5	40.3	839	US-09-197-636-8	Sequence 8, Appl
12	1556.5	40.3	839	US-09-235-451-34	Sequence 34, Appl
13	1556.5	40.3	839	US-09-978-303-34	Sequence 34, Appl
14	1555.5	40.3	839	US-09-533-220A-2	Sequence 2, Appl
15	1555.5	40.3	839	US-09-949-016-6937	Sequence 6937, Ap
16	1552.5	40.2	839	US-09-197-636-4	Sequence 4, Appl
17	1551.5	40.2	839	US-09-667-422-4	Sequence 4, Appl
18	1375	35.6	798	US-09-949-016-9926	Sequence 9926, Ap
19	1324	34.3	761	US-09-235-451-4	Sequence 4, Appl
20	1324	34.3	761	US-09-978-303-4	Sequence 4, Appl
21	1306	33.9	889	US-09-132-316-2	Sequence 2, Appl
22	1298.5	33.7	764	US-09-235-451-36	Sequence 36, Appl
23	1298.5	33.7	764	US-09-978-303-36	Sequence 36, Appl
24	1071	27.8	511	US-09-667-422-5	Sequence 5, Appl
25	777	20.1	727	US-09-235-451-23	Sequence 23, Appl
26	777	20.1	727	US-09-978-303-23	Sequence 23, Appl
27	733	19.0	727	US-09-350-457A-4	Sequence 4, Appl

28	724.5	18.8	725	4	US-09-350-457A-2	Sequence 2, Appl
29	548.5	14.2	279	4	US-09-149-476-500	Sequence 500, App
30	521	13.5	511	4	US-09-759-143-909	Sequence 909, App
31	227	5.9	71	3	US-09-235-451-14	Sequence 14, Appl
32	227	5.9	71	4	US-09-978-303-14	Sequence 14, Appl
33	221.5	5.7	1709	4	US-09-392-812A-6	Sequence 6, Appl
34	216	5.6	1165	4	US-09-949-016-6874	Sequence 6874, Ap
35	215	5.6	1165	4	US-09-949-016-11392	Sequence 11392, A
36	213	5.5	134	4	US-09-759-143-910	Sequence 910, App
37	210	5.4	1619	4	US-09-392-812A-4	Sequence 4, Appl
38	180	4.7	1704	4	US-09-392-812A-2	Sequence 2, Appl
39	172	4.5	1095	3	US-09-112-096-15	Sequence 15, Appl
40	172	4.5	1095	4	US-09-636-215-778	Sequence 778, App
41	172	4.5	1095	4	US-09-685-166A-778	Sequence 778, App
42	172	4.5	1095	4	US-09-679-426-778	Sequence 778, App
43	172	4.5	1095	4	US-09-759-143-778	Sequence 778, App
44	172	4.5	1095	4	US-09-651-236-778	Sequence 778, App
45	169	4.4	1095	4	US-09-636-215-780	Sequence 780, App

ALIGNMENTS

RESULT 1

US-09-500-123-12

; Sequence 12, Application US/09500123

; Patent No. 6455278

; GENERAL INFORMATION:

; APPLICANT: Dubin, Adrienne E

; APPLICANT: Huvar, Arne

; APPLICANT: Erlander, Mark G

; APPLICANT: Glass, Charles A

; TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor

; TITLE OF INVENTION: VR3

; FILE REFERENCE: Human VR3 receptors

; CURRENT APPLICATION NUMBER: US/09/500,123

; CURRENT FILING DATE: 2000-02-08

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 12

; LENGTH: 742

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-500-123-12

Query Match		100.0%;	Score 3858;	DB 4;	Length 742;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 742;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MADSEGPAGPGEVAELPGDESGTGGGEAFPLSSLANLFEDEGSLSPADASRPAGP	60		
Db	1	MADSEGPAGPGEVAELPGDESGTGGGEAFPLSSLANLFEDEGSLSPADASRPAGP	60		
Qy	61	GDGRNLRMKQAGAPRKGVNPIDILLESITYESSVVPKAPMDSLFYGYRHHSSN	120		
Db	61	GDGRNLRMKQAGAPRKGVNPIDILLESITYESSVVPKAPMDSLFYGYRHHSSN	120		
Qy	121	KWRKKITTEKQPOSQAPAPPPPILKVFNPILFDIVSRGSTADLDGLPLLLTHKKKL	180		
Db	121	KWRKKITTEKQPOSQAPAPPPPILKVFNPILFDIVSRGSTADLDGLPLLLTHKKKL	180		
Qy	181	TDEEPREPTGKTCPLKALLNLSNGRNTIPVLLDIAERTGNMREFFINSPPFDIYRGQT	240		
Db	181	TDEEPREPTGKTCPLKALLNLSNGRNTIPVLLDIAERTGNMREFFINSPPFDIYRGQT	240		
Qy	241	ALHIAIERCKHYVELLVAQADVHAQARFPQPKDEGGYFYFGEPLSLAECTNQPHI	300		
Db	241	ALHIAIERCKHYVELLVAQADVHAQARFPQPKDEGGYFYFGEPLSLAECTNQPHI	300		
Qy	301	VNYLTENPHKADMRQDSRGNTVLHALVADNTRENTKFTVKMDVLLLLKCARLFPDS	360		
Db	301	VNYLTENPHKADMRQDSRGNTVLHALVADNTRENTKFTVKMDVLLLLKCARLFPDS	360		

QY 361 NLEAVLNNDGLSPLMAAATGKIGIFQHIIIRREVTDDETRHLSRKFKDWAYGVPVSSLYD 420
DB 361 NLEAVLNNDGLSPLMAAATGKIGIFQHIIIRREVTDDETRHLSRKFKDWAYGVPVSSLYD 420
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINNVSYLC 480
DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINNVSYLC 480
QY 481 AMVIFTLTAYYQPLGTPPYRTTVDYLRAGEVITLFTGVLFFFTNIKOLFMMKCPGV 540
DB 481 AMVIFTLTAYYQPLGTPPYRTTVDYLRAGEVITLFTGVLFFFTNIKOLFMMKCPGV 540
QY 541 NSLFDGSPQLLYFYISVLIVSAALYLAGIEAYLAVMVFALVGMNALLYFTRGKLTG 600
DB 541 NSLFDGSPQLLYFYISVLIVSAALYLAGIEAYLAVMVFALVGMNALLYFTRGKLTG 600
QY 601 TYSIMIQILFKDLFRLLVYLLFMIGYASALVSLNPCANNKVCNEQDCTNCTVTPYPS 660
DB 601 TYSIMIQILFKDLFRLLVYLLFMIGYASALVSLNPCANNKVCNEQDCTNCTVTPYPS 660
QY 661 RDSEFTFSLDLFKLTGMDLEMLSTKYPVVFIIILLVTVIILTFVLLNMLIALMGE 720
DB 661 RDSEFTFSLDLFKLTGMDLEMLSTKYPVVFIIILLVTVIILTFVLLNMLIALMGE 720
QY 721 TVGOVSKESKHIWKLQSGRRRL 742
DB 721 TVGOVSKESKHIWKLQSGRRRL 742

RESULT 2

US-09-500-123-7

; Sequence 7, Application US/09500123

; Patent No. 6455278

; GENERAL INFORMATION:

; APPLICANT: Dubin, Adrienne E

; APPLICANT: Huvar, Arne

; APPLICANT: Erlander, Mark G

; APPLICANT: Glass, Charles A

; TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor

; FILE REFERENCE: Human VR3

; CURRENT APPLICATION NUMBER: US/09/500,123

; CURRENT FILING DATE: 2000-02-08

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 871

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-500-123-7

Query Match 99.1%; Score 3823; DB 4; Length 871;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 735; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MADSEGPAGGGEVAELPGDESGTPGGEAPPLSLANLFEDEGSLSPADASRRPAGP 60
DB 1 MADSEGPAGGGEVAELPGDESGTPGGEAPPLSLANLFEDEGSLSPADASRRPAGP 60
QY 61 GDGRPNLRMKFQGAFRKGVNPNIDLLESTLYESSVVPKAPMDSLFDYGYRHHSSDN 120
DB 61 GDGRPNLRMKFQGAFRKGVNPNIDLLESTLYESSVVPKAPMDSLFDYGYRHHSSDN 120
QY 121 KRWKRIIEKQPSKAPAPQPPPIKVFNRPIILFDIVSRGSTADLGLLFFLTHKKRL 180
DB 121 KRWKRIIEKQPSKAPAPQPPPIKVFNRPIILFDIVSRGSTADLGLLFFLTHKKRL 180
QY 181 TDEFRPSTGKTCPLKALLNSGRNDTI PVLLDIAERTGNMREFINSPRDIYRGQT 240
DB 181 TDEFRPSTGKTCPLKALLNSGRNDTI PVLLDIAERTGNMREFINSPRDIYRGQT 240
QY 241 ALHIAIERRCHYVELLVAQADVHAQGRFFQPKDEGGYFFGELPLSLAACTNQPHI 300

DB 241 ALHIAIERRCHYVELLVAQADVHAQGRFFQPKDEGGYFFGELPLSLAACTNQPHI 300
QY 301 VNYLTENPHKADMRQDSRGNTVLHALVAIADNTRENTKFVTKMYDILLKLCARLFPDS 360
DB 301 VNYLTENPHKADMRQDSRGNTVLHALVAIADNTRENTKFVTKMYDILLKLCARLFPDS 360
QY 361 NLEAVLNNDGLSPLMAAATGKIGIFQHIIIRREVTDDETRHLSRKFKDWAYGVPVSSLYD 420
DB 361 NLEAVLNNDGLSPLMAAATGKIGIFQHIIIRREVTDDETRHLSRKFKDWAYGVPVSSLYD 420
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINNVSYLC 480
DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINNVSYLC 480
QY 481 AMVIFTLTAYYQPLGTPPYRTTVDYLRAGEVITLFTGVLFFFTNIKOLFMMKCPGV 540
DB 481 AMVIFTLTAYYQPLGTPPYRTTVDYLRAGEVITLFTGVLFFFTNIKOLFMMKCPGV 540
QY 541 NSLFDGSPQLLYFYISVLIVSAALYLAGIEAYLAVMVFALVGMNALLYFTRGKLTG 600
DB 541 NSLFDGSPQLLYFYISVLIVSAALYLAGIEAYLAVMVFALVGMNALLYFTRGKLTG 600
QY 601 TYSIMIQILFKDLFRLLVYLLFMIGYASALVSLNPCANNKVCNEQDCTNCTVTPYPS 660
DB 601 TYSIMIQILFKDLFRLLVYLLFMIGYASALVSLNPCANNKVCNEQDCTNCTVTPYPS 660
QY 661 RDSEFTFSLDLFKLTGMDLEMLSTKYPVVFIIILLVTVIILTFVLLNMLIALMGE 720
DB 661 RDSEFTFSLDLFKLTGMDLEMLSTKYPVVFIIILLVTVIILTFVLLNMLIALMGE 720
QY 721 TVGOVSKESKHIWKLQ 736
DB 721 TVGOVSKESKHIWKLQ 736

RESULT 3

US-09-500-123-9

; Sequence 9, Application US/09500123

; Patent No. 6455278

; GENERAL INFORMATION:

; APPLICANT: Dubin, Adrienne E

; APPLICANT: Huvar, Arne

; APPLICANT: Erlander, Mark G

; APPLICANT: Glass, Charles A

; TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor

; FILE REFERENCE: Human VR3

; CURRENT APPLICATION NUMBER: US/09/500,123

; CURRENT FILING DATE: 2000-02-08

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 9

; LENGTH: 811

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-500-123-9

Query Match 89.9%; Score 3470; DB 4; Length 811;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 675; Conservative 0; Mismatches 1; Indels 60; Gaps 1;

QY 1 MADSEGPAGGGEVAELPGDESGTPGGEAPPLSLANLFEDEGSLSPADASRRPAGP 60
DB 1 MADSEGPAGGGEVAELPGDESGTPGGEAPPLSLANLFEDEGSLSPADASRRPAGP 60
QY 61 GDGRPNLRMKFQGAFRKGVNPNIDLLESTLYESSVVPKAPMDSLFDYGYRHHSSDN 120
DB 61 GDGRPNLRMKFQGAFRKGVNPNIDLLESTLYESSVVPKAPMDSLFDYGYRHHSSDN 120
QY 121 KRWKRIIEKQPSKAPAPQPPPIKVFNRPIILFDIVSRGSTADLGLLFFLTHKKRL 180
DB 121 KRWKRIIEKQPSKAPAPQPPPIKVFNRPIILFDIVSRGSTADLGLLFFLTHKKRL 180


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QY 181 TDEPREPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOT 240
Db 181 TDEPREPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOT 240
QY 241 ALHIAIERRCHYVELLVAQAGADVHAQARGFQPKDEGGYFYFGEPLSLAACTNQPHI 300
Db 241 ALHIAIERRCHYVELLVAQAGADVHAQARGFQPKDEGGYFYFGEPLSLAACTNQPHI 300
QY 301 VNYLTENPHKKADMERQDSRGNTVILHALVAIADNTRENTKFTVMYDLLLLKCARLFPDS 360
Db 301 VNYLTENPHKKADMERQDSRGNTVILHALVAIADNTRENTKFTVMYDLLLLKCARLFPDS 360
QY 361 NLEAVLNNDGLSPLMAAKTKIGIFQHIIRREVTDTRHLRSRKFQWAYGVVSYLYD 420
Db 361 NLEAVLNNDGLSPLMAAKTK----- 381
QY 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYL 480
Db 421 -----KIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYL 420
QY 481 AMVIFTLTAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLPFTTNIKOLFMMKKCPGV 540
Db 421 AMVIFTLTAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLPFTTNIKOLFMMKKCPGV 480
QY 541 NSLFDGSQLLYFYISVILVISAALYLAGIAYLAVMVVALVGLWMNALYFTRGLKLTG 600
Db 481 NSLFDGSQLLYFYISVILVISAALYLAGIAYLAVMVVALVGLWMNALYFTRGLKLTG 540
QY 601 TYSIMOKILFKDLFRLLVLLFMIGVASALVSLNPNCAKMKVNEOTNCTVPTPSC 660
Db 541 TYSIMOKILFKDLFRLLVLLFMIGVASALVSLNPNCAKMKVNEOTNCTVPTPSC 600
QY 661 RDSEFTSFLLDLFKLTGMDLEMLSSTKYPVFIILLVTVIILTFVLLNMLALMGE 720
Db 601 RDSEFTSFLLDLFKLTGMDLEMLSSTKYPVFIILLVTVIILTFVLLNMLALMGE 660
QY 721 TVGQVSKESKHIWKLO 736
Db 661 TVGQVSKESKHIWKLO 676

RESULT 4
US-09-235-451-25
; Sequence 25, Application US/09235451
; GENERAL INFORMATION:
; APPLICANT: Caterina, David J.
; APPLICANT: Caterina, Michael J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
; FILE REFERENCE: 9076/084CIP
; CURRENT APPLICATION NUMBER: US/09/235,451
; CURRENT FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 843
; ORGANISM: chicken
US-09-235-451-25

Query Match 41.6%; Score 1604.5; DB 3; Length 843;
Best Local Similarity 47.5%; Pred. No. 1.4e-143;
Matches 343; Conservative 128; Mismatches 184; Indels 67; Gaps 18;

QY 41 EGEDSGLSPADARPGDGRNLRMKFGARFKGVNPDIDLESTLY--ESSVPG 98
Db 27 DGEDSAL--ETAD-----NLQGT-----SNKVQPSKSNIFARRGRFVNG 64

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QY 99 ---PKKAMPDLSFY-----GTVRHSSDNKRWRKKIIEKQP-----QSPKAPAPOPPPIL 146
Db 65 DCDKDMAPDMSFYQWDHLMAPSVIKFHAMMERGLKHLSTDSITGCSKA-----F 116
QY 147 KVFVRPILFDIVSRGSTADLOGLLPFLTHKKRLTDEEFREPSCTKCLPKALLNSGR 206
Db 117 KEYDRRIRFDVARGSTKDLDDLLYLNRTLKLHLDDEFEKPECTKCTCLLKAMLNHDK 176
QY 207 NDTIPVLIDIAERTGNMREFINSPFRDIYRGQTAHIAIERRCHYVELLVAQAGADVHA 266
Db 177 NDTIPVLIDIAERTGNMREFINSPFRDIYRGQTAHIAIERRCHYVELLVAQAGADVHA 236
QY 267 QARGRFPQ-KDEGGYFYFGEPLSLAACTNQPHIVNYLTENPHKKADMERQDSRGNTV 325
Db 237 RACGEFFRKIKGPG-FYFGEPLSLAACTNQPCIVKLEENPYQAADIAEDSMGMVL 295
QY 326 HALVAIADNTRENTKFTVMYDLLLLKCARLFPDSNLEAVLNNDGLSPLMAAKTKIGI 385
Db 296 HTLVEIADNTKDNFTVMYNNILILGAKINPLIKLEELTNKKGLTFLTLAAKTKIGI 355
QY 386 FOHIIRREVTDTRHLRSRKFQWAYGVVSYLYDLSSLDTCGEEASVLEILVYNSKIEN 445
Db 356 PAYILRREIKDPECHLSRKTETWAYGVHSLYDLSCIDTC-EKNSVLEIITAYSETPN 414
QY 446 RHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLCAVIFTLTAYYQPLE--GTTPPY 502
Db 415 RHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLCAVIFTLTAYYQPLE--GTTPPY 474
QY 503 RTVDYLRAGEVITLFTGVLPFTTNIKOLFMMKKCPGVNSLFDGSQLLYFYISVILV 562
Db 475 HSTGEYFRTVEIILSVLGLYFFRGIQ-YFVORRPSLKTIVDSYSEVLPFVHSLLS 533
QY 563 SAALYLAGIAYLAVMVVALVGLWMNALYFTRGLKLTGYSIMOKILFKDLFRLLVYL 622
Db 534 SVLVYFCQELVYASWFSALGHWANMLYTRGFMQNGIYSVIAKWLIRDLCRPMFVYL 593
QY 623 LFMIGYASALVSLNPNCAKMKVNEOTNCTVPTPSCRDSEFT-----FLDLF 674
Db 594 VLLGFSSTAVTLIED-----DNEGQDTNSS--EYARCSHTKRGRTSYNSLYYTCLEUF 645
QY 675 KLTGMDLEMLSSTKYPVFIILLVTVIILTFVLLNMLALMGETVQVSKESKHIWK 734
Db 646 KFTIGMDLEFTENYRPSKSVFVILLVLYVILTYILLNMLALMGETVSKIAQESKSIWK 705
QY 735 LQ 736
Db 706 LQ 707

RESULT 5
US-09-978-303-25
; Sequence 25, Application US/09978303
; Patent No. 6790629
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: Nucleic acid sequences encoding
; TITLE OF INVENTION: capsaicin receptor and capsaicin receptor-related
; FILE REFERENCE: UCAL084CON
; CURRENT APPLICATION NUMBER: US/09/978,303
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25

```


Sequence 3, Application US/09132316B
Patent No. 6444440
GENERAL INFORMATION:
APPLICANT: Young, Paul E.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Vanilloid Receptor-2
FILE REFERENCE: 1488.1110000
CURRENT APPLICATION NUMBER: US/09/132,316B
CURRENT FILING DATE: 1998-08-11
EARLIER APPLICATION NUMBER: US 60/040,163
EARLIER FILING DATE: 1997-03-07
PCT/US98/04493
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 3
LENGTH: 838
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-132-316-3

Query Match 40.9%; Score 1579.5; DB 4; Length 838;
Best Local Similarity 44.6%; Pred. No. 3.3e-141;
Matches 338; Conservative 129; Mismatches 193; Indels 97; Gaps 16;

QY 16 AELPDGDESGTGCGE-----AFPLSSLANLFEGEDGSLSPSPADA 54
DB 5 ASLDESESESPQENSCLDPPDRDNCPPPPVKPHFTTRSTRLF-GKGDSEASPLDC 63
QY 55 SRPAGPGDGRPNLRMKFQAGFRKGVN-PIDLLESTLYESSVVPKPKAPMDSLFDYGY 113
DB 64 PYEEG-----GLASCPITVSSVL-----TIQPGDGP-----ASV 94
QY 114 RHSSDNKRWKRIIEKQPSKAPAPQPPPIKLVFNRPILFDIVSRGSTADLGLLPL 173
DB 95 RPSSQDS-----VSAGEKPP--RLYDRRSIFDAVAQSCQESLPL 136
QY 174 LTHKKRLTDEEPREPSTGKTCLPKALLNLSGRNDTIPVLLDIAERTGNMRBFINSPPRD 233
DB 137 QRSKRLTDSFEDKDETGTCLLKAMLNHNGQNTIALLDVARKTSLKGFVNASTD 196
QY 234 IYRGQTALHIAIERCKHYVELLVAQADVHAQAGRFQPKDEGGYFYFGEPLSLAA 293
DB 197 SYKGQTALHIAIERNNMTLVLLVENGADVQAAANGOFFKTKGRPGFYFGEPLSLAA 256
QY 294 CTNQPHIVNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLK 353
DB 257 CTNQLAIVKFLQNSWQPADISARDSVGNVTVLHALVEADNTVDNTKFTVSMYNEILIG 316
QY 354 ARLPDPSNLEAVLNNDGLSPLMMAKTGKIGIFOHIIREVTVDEDTLHLSRKFKDWAYGP 413
DB 317 AKLHPTLKEETNRKGLTPLALAASSGKIGVLAYILOREIHEPECRHLISRFTWAYGP 376
QY 414 VYSSLYDLSLDTCCGEASVLEILVY-NSKIENRHEMLAVEPINELLRDKRWKFGAVSFY 472
DB 377 VHSSLYDLSIDTC-EKNSVLEVIAYSSSETNRHDMLLVEPLNRLQDKWDFVKRIFY 435
QY 473 INVSVLCAMVIFTLTAYYQPLEGTPPYRTTV-DYLRAGEVITLFTGVLFFFTNKID 531
DB 436 FNFFVYCLYMIIFTAAAYRPPVEGLPPYKLNVTGDFRVTGEILSVSGGVYFFFRGIQ- 494
QY 532 LPMKCPGNSIFDGSFOLLFYISVLVISAALYLAGIEAYLAVMVPALVGLHNMNLY 591
DB 495 YFLQRRPSLKSFLVDSYSBILFFVQSLFVLVSVLYFSQKKEYVASWFLANGWTNMLY 554
QY 592 FTRGLKLTGYIMIQKILFDLFRFLLYLLFMIGYASALVSLNCPKAMKVCNEDQTN 651
DB 555 YTRGQMGYIYAVMIEKMIIRDLCRFMFVYLVFLGFSFVAVTLI-----EDGKN 604
QY 652 CTVP---TVPSCRDS-----ETFSFTLDDLKLTIGMGDLEMLSTKYPVVFILL 699
DB 605 NSLPMESTPHKRCGSACKPGNSYNSLYST-CLELPKFTIGMGDLFTENYDFKAVFIILL 663

QY 700 VTYIILTFVLLNMLIALMGETVGVQVSKESKHIWKLO 736
DB 664 LAYVILTIVLLNMLIALMGETVNVKIAQESKNIWKLO 700

RESULT 8
US-09-667-422-9
Sequence 9, Application US/09667422
Patent No. 6482611
GENERAL INFORMATION:
APPLICANT: Cortright, Daniel
APPLICANT: Krause, James
TITLE OF INVENTION: Human Capsaicin Receptor and Uses Thereof
FILE REFERENCE: HCR
CURRENT APPLICATION NUMBER: US/09/667,422
CURRENT FILING DATE: 2001-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 9
LENGTH: 838
TYPE: PRT
ORGANISM: Rattus sp.
PUBLICATION INFORMATION:
AUTHORS: Caterina, Michael J.
AUTHORS: Schumacher, Mark A.
AUTHORS: Tominaga, Makoto
AUTHORS: Rosen, Tobias A.
TITLE: The capsaicin receptor: a heat-activated ion channel in
TITLE: the pain pathway
JOURNAL: Nature
VOLUME: 389
PAGES: 816-824
DATE: 1997
US-09-667-422-9

Query Match 40.9%; Score 1579.5; DB 4; Length 838;
Best Local Similarity 44.6%; Pred. No. 3.3e-141;
Matches 338; Conservative 129; Mismatches 193; Indels 97; Gaps 16;

QY 16 AELPDGDESGTGCGE-----AFPLSSLANLFEGEDGSLSPSPADA 54
DB 5 ASLDESESESPQENSCLDPPDRDNCPPPPVKPHFTTRSTRLF-GKGDSEASPLDC 63
QY 55 SRPAGPGDGRPNLRMKFQAGFRKGVN-PIDLLESTLYESSVVPKPKAPMDSLFDYGY 113
DB 64 PYEEG-----GLASCPITVSSVL-----TIQPGDGP-----ASV 94
QY 114 RHSSDNKRWKRIIEKQPSKAPAPQPPPIKLVFNRPILFDIVSRGSTADLGLLPL 173
DB 95 RPSSQDS-----VSAGEKPP--RLYDRRSIFDAVAQSCQESLPL 136
QY 174 LTHKKRLTDEEPREPSTGKTCLPKALLNLSGRNDTIPVLLDIAERTGNMRBFINSPPRD 233
DB 137 QRSKRLTDSFEDKDETGTCLLKAMLNHNGQNTIALLDVARKTSLKGFVNASTD 196
QY 234 IYRGQTALHIAIERCKHYVELLVAQADVHAQAGRFQPKDEGGYFYFGEPLSLAA 293
DB 197 SYKGQTALHIAIERNNMTLVLLVENGADVQAAANGOFFKTKGRPGFYFGEPLSLAA 256
QY 294 CTNQPHIVNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLK 353
DB 257 CTNQLAIVKFLQNSWQPADISARDSVGNVTVLHALVEADNTVDNTKFTVSMYNEILIG 316
QY 354 ARLPDPSNLEAVLNNDGLSPLMMAKTGKIGIFOHIIREVTVDEDTLHLSRKFKDWAYGP 413
DB 317 AKLHPTLKEETNRKGLTPLALAASSGKIGVLAYILOREIHEPECRHLISRFTWAYGP 376
QY 414 VYSSLYDLSLDTCCGEASVLEILVY-NSKIENRHEMLAVEPINELLRDKRWKFGAVSFY 472
DB 377 VHSSLYDLSIDTC-EKNSVLEVIAYSSSETNRHDMLLVEPLNRLQDKWDFVKRIFY 435
QY 473 INVSVLCAMVIFTLTAYYQPLEGTPPYRTTV-DYLRAGEVITLFTGVLFFFTNKID 531

Db 436 ENFFVYCLYMIIFTAAAYRPPVEGLPPYKXNTVGDYFRTVTEILSVSGVYFFFRGIQ- 494
QY 532 LFMKCPGVNSLFDGSPQLLYFYIYVSVLYVISAALYLAGIAYLAVMVFALVGLWMNLY 591
Db 495 YFLQRRPSLKSFLVDSYSEILFFVQSLFMLSVVLYFSQKEYVASMVFSLAMGWTNMLY 554
QY 592 FTRGLKLTGTYSIMQKILFKDLFRFLAVYLLFMIGYASALVSLNPCANMKVCNEDQTN 651
Db 555 YTRGFQQMGITVAVMIERKMLRDLRCFMEFVYLVFLFGFSTAVVTLL-EDGKN 604
QY 652 CTVP---TYPSCRDS-----ETFTFLDLFKLTIGMDLEMLSTKYPPVVFIILL 699
Db 605 NSLPWESTPHKCRGSACKPGNSYSLYST-CLELFKFTIGMDLEFTENYDEKAVFIILL 663
QY 700 VTYIILTFVLLNMLIALMGSETVQGVSKESKHIWKLQ 736
Db 664 LAYVILTAYLLNMLIALMGSETVQGVSKESKHIWKLQ 700

RESULT 9
US-09-978-303-2
; Sequence 2, Application US/09978303
; Patent No. 6790629
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: Nucleic acid sequences encoding
; TITLE OF INVENTION: capsalain receptor and capsalain receptor-related
; TITLE OF INVENTION: polypeptides and uses thereof
; FILE REFERENCE: UCAL084CON
; CURRENT APPLICATION NUMBER: US/09/978,303
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 838
; TYPE: PRT
; ORGANISM: R. rattus
US-09-978-303-2

Query Match 40.9%; Score 1579.5; DB 4; Length 838;
Best Local Similarity 44.6%; Pred. No. 3.3e-141;
Matches 338; Conservative 129; Mismatches 193; Indels 97; Gaps 16;
QY 16 AELPDGSGTGGGE-----APPLSLANLFEEDGSLSPSPADA 54
Db 5 ASLDSSESPQENSCILDPDRDPNCKPPVPKPHFTTRSRTRLF-KGSDSEASPLDC 63
QY 55 SRPAGPGGRNLRMKFGARFKGVPN-PIDLLSTLYESSVWPGKAPMDSLFDYCTY 113
Db 64 PYEG-----GLASCIITVSSVL-----TIQPGDGP-----ASV 94
QY 114 RHGSDNKRKKIIEKQSPKAPAPQPPILKVNRPILFDIVSRGSTADLDGLPFL 173
Db 95 RPSSQDS-----VSAGEKPP-RLYDRSIFDAVAQSNQCELESLLPFL 136
QY 174 LTHKGLTDEFRPSTGKTLCPKALLNLSGRNDTIPIVLDIAERTGNWREFINSPPRD 233
Db 137 QRSKRLTDSFQKOPETGKTLCKLAMLNLHGNDTIALLDLVARKTDSLKQFVNASTD 196
QY 234 IYRGOTALHAIERCKHYVELLVAQADYHAQGRFFQPKDBGGYFYGELPLSLAA 293
Db 197 SYKQOTALHAIERNMTLVLLVENGADYQAANGDFPKTKGRPGFYFGEPLSLAA 256
QY 294 CTNQPHIVNYLTENPHKADNRQDSRQNTVNLHALVAIADNTRENTKFTVTKYDILLK 353

Db 257 CTNQLAIKVFLLQNSQPADISARDSVGNVTVLHALVEVADNTVNTKFTVSMYNEILLG 316
QY 354 ARLFPDSNLEAVLNNDGLSPMLMAAKTKIGIFQHIIRREVTDTRHLRKRKFDWAYGP 413
Db 317 AKLHPTLKLBEITNRKGLTPLALAASSGKIGVLAYLQRETHEPECRHLRKRFTWAYGP 376
QY 414 VYSSLYDLSLDTCCGEASVLEILVY-NSKIENRHEMLAVEPINELLARDKWRKFAVGFY 472
Db 377 VHSSLYDLSLDTCC-ERKNSVLEIYAYSSSTFNRHDMILLVEPLNRLLQOKRDFVKRIFY 435
QY 473 INVSYLCAMVIFTLTAYYQPLEGTPPYPTTV-DYLRLAGEVITLFTGLVFFFTNKD 531
Db 436 ENFFVYCLYMIIFTAAAYRPPVEGLPPYKXNTVGDYFRTVTEILSVSGVYFFFRGIQ- 494
QY 532 LFMKCPGVNSLFDGSPQLLYFYIYVSVLYVISAALYLAGIAYLAVMVFALVGLWMNLY 591
Db 495 YFLQRRPSLKSFLVDSYSEILFFVQSLFMLSVVLYFSQKEYVASMVFSLAMGWTNMLY 554
QY 592 FTRGLKLTGTYSIMQKILFKDLFRFLAVYLLFMIGYASALVSLNPCANMKVCNEDQTN 651
Db 555 YTRGFQQMGITVAVMIERKMLRDLRCFMEFVYLVFLFGFSTAVVTLL-EDGKN 604
QY 652 CTVP---TYPSCRDS-----ETFTFLDLFKLTIGMDLEMLSTKYPPVVFIILL 699
Db 605 NSLPWESTPHKCRGSACKPGNSYSLYST-CLELFKFTIGMDLEFTENYDEKAVFIILL 663
QY 700 VTYIILTFVLLNMLIALMGSETVQGVSKESKHIWKLQ 736
Db 664 LAYVILTAYLLNMLIALMGSETVQGVSKESKHIWKLQ 700

RESULT 10
US-09-197-636-2
; Sequence 2, Application US/09197636
; Patent No. 6239267
; GENERAL INFORMATION:
; APPLICANT: DUCKWORTH, DAVID
; APPLICANT: HAYES, PHILIP
; APPLICANT: MEADOWS, HELEN
; APPLICANT: DAVIS, JOHN
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: US
; ZIP: 19482-0980
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/197,636
; FILING DATE: 23-NOV-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 9805137.8
; FILING DATE: 12-MAR-1998
; APPLICATION NUMBER: UK 9815791.0
; FILING DATE: 21-JUL-1998
; APPLICATION NUMBER: UK 9819278.4
; FILING DATE: 03-SEP-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-30075
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 601-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169

; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 839 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-197-636-2

Query Match 40.4%; Score 1557.5; DB 3; Length 839;
 Best Local Similarity 44.5%; Pred No. 4.1e-139;
 Matches 321; Conservative 138; Mismatches 188; Indels 74; Gaps 12;

QY	49	PSPADSRPAGDGRPNL-----RMKFGQ-----AFKGVNPNIDLLS--TLYESSV	95
DB	22	FDPLDGDNSRPPPAKPOLSTAKSRTRLFKGDSEAPVDCPHEGELDSCTTITVSPV	81
QY	96	V-----PGPKAPMWSLFDYGYTRHSSDNKRWRKKIIKQPPSPKAPAPQPPILKVF	149
DB	82	ITIQRPDGPFGARL-----LSQDSVAASSTKTLRLY	113
QY	150	NRPIFDIVSRGSTADLGLLPFLTHKKRLTDEEFREPSTGKTCCLKPALLNLSNGRNDT	209
DB	114	DRSIFEVAQNQCDELLELFLQSKXHLTDNEFKDPETGKTCCLKAMLNHLHGQNTT	173
QY	210	IPVLDDIAERTGNMREFINSPRDIYYRGQTALHIAIERRCCKHYVELLVQAQADVHAQAR	269
DB	174	IPLLLEIARQDSLKELVNASYDTSYKGTALHIAIERRNALVTLLVENGADVQAAAH	233
QY	270	GRFPQKDEGGYFYFGEPLSLAACTNQHIVNYLTENPHKKADMRRDORSGNTVLHALV	329
DB	234	GDFFKTKRGPRGFGYFGEPLSLAACTNQLGIVKFLQNSWQTADISARDSVGNVTVLHALV	293
QY	330	AIADNTRENTKFTVKMYDILLKLCARLPDPSNLEAVLNDGLSLPLMAAKTKGIGFOHI	389
DB	294	EVAADNTADNTKFTVMSYMEIILGAKLHPTLKLBELTNKKGMTPLAAGTKIGVLAYI	353
QY	390	IRREVTDBDTRHLSRKFWDWAYGVPYSSLYDLSSLDTCGEASVLEILVY-NSKIENRHE	448
DB	354	LOREIQEPECHLSRKFTEWAYGPHSSLYDLSCIDTC-EKNSVLEIAYSSSETPNRHD	412
QY	449	MLAEPINELLRDKWRKFGVSYINVSYLCAWVIFLTAYYQPLEGTPPYPRYTTVDY	508
DB	413	MLLVEPLNRLQDKWDRFVKRIFYENFLVYCLYMIIFTMAAYRPRVDGLPFPKMEKTGDY	472
QY	509	LRLAGEVITLFTGVLFFFTNIKDLFWKPCGVNSLFDIGSQFLLYFYISLVIVSAAALYL	568
DB	473	FRVTGEILSVLGVYFFFRGIGQ-YFLQRRPMSKTLFVDSYSMLFFLQSLFMLATVLYLF	531
QY	569	AGIEAYLAVMVFALVGLWNNALYFTRGLKLTGYISIMIQKILFKDLFRFLAVYLLFMIGY	628
DB	532	SHLKEYVASMVPSLALGWTNMLYTRGQOMGIYAVMEIKMLRLDLCRFMFYIYVFLFGP	591
QY	629	ASALVSLNPNCAVMKVNEDQNTCTVPTVY-----PSCRDSST-----PSTFLLDLPK	675
DB	592	STAVVTLLI-----EDGKNDLSPESTSHRWGRPACRPDPSYNSLYST-CLELFPK	640
QY	676	LTIGMGDLEMLSSSTKYPVVFILLTYLTFTVLLNMLIALMGSETVQGVSKESGHIWKL	735
DB	641	FTIGMGDLEFTENYDFKAVFIILLAYLYLTLYILLNMLIALMGSETVKNKIAQESKNWKL	700
QY	736	Q 736	
DB	701	Q 701	

RESULT 11
 US-09-197-636-8
 ; Sequence 8, Application US/09197636
 ; Patent No. 6239267
 ; GENERAL INFORMATION:
 ; APPLICANT: DUCKWORTH, DAVID
 ; APPLICANT: HAYES, PHILIP

; APPLICANT: MEADOWS, HELEN
 ; APPLICANT: DAVIS, JOHN
 ; TITLE OF INVENTION: NOVEL COMPOUNDS
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Ratner & Prestia
 ; STREET: P.O. Box 980
 ; CITY: Valley Forge
 ; STATE: PA
 ; COUNTRY: US
 ; ZIP: 19482-0980
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/197,636
 ; FILING DATE: 23-NOV-1998
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: UK 9805137.8
 ; FILING DATE: 12-MAR-1998
 ; APPLICATION NUMBER: UK 9815791.0
 ; FILING DATE: 21-JUL-1998
 ; APPLICATION NUMBER: UK 9819278.4
 ; FILING DATE: 03-SEP-1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Prestia, Paul F
 ; REGISTRATION NUMBER: 23,031
 ; REFERENCE/DOCKET NUMBER: GP-30075
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 601-407-0700
 ; TELEFAX: 610-407-0701
 ; TELEX: 846169
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 839 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-197-636-8

Query Match 40.3%; Score 1556.5; DB 3; Length 839;
 Best Local Similarity 44.5%; Pred No. 5.1e-139;
 Matches 321; Conservative 138; Mismatches 188; Indels 74; Gaps 12;

QY	49	PSPADSRPAGDGRPNL-----RMKFGQ-----AFKGVNPNIDLLS--TLYESSV	95
DB	22	FDPLDGDNSRPPPAKPOLSTAKSRTRLFKGDSEAPVDCPHEGELDSCTTITVSPV	81
QY	96	V-----PGPKAPMWSLFDYGYTRHSSDNKRWRKKIIKQPPSPKAPAPQPPILKVF	149
DB	82	ITIQRPDGPFGARL-----LSQDSVAASSTKTLRLY	113
QY	150	NRPIFDIVSRGSTADLGLLPFLTHKKRLTDEEFREPSTGKTCCLKPALLNLSNGRNDT	209
DB	114	DRSIFEVAQNQCDELLELFLQSKXHLTDNEFKDPETGKTCCLKAMLNHLHGQNTT	173
QY	210	IPVLDDIAERTGNMREFINSPRDIYYRGQTALHIAIERRCCKHYVELLVQAQADVHAQAR	269
DB	174	IPLLLEIARQDSLKELVNASYDTSYKGTALHIAIERRNALVTLLVENGADVQAAAH	233
QY	270	GRFPQKDEGGYFYFGEPLSLAACTNQHIVNYLTENPHKKADMRRDORSGNTVLHALV	329
DB	234	GDFFKTKRGPRGFGYFGEPLSLAACTNQLGIVKFLQNSWQTADISARDSVGNVTVLHALV	293
QY	330	AIADNTRENTKFTVKMYDILLKLCARLPDPSNLEAVLNDGLSLPLMAAKTKGIGFOHI	389
DB	294	EVAADNTADNTKFTVMSYMEIILGAKLHPTLKLBELTNKKGMTPLAAGTKIGVLAYI	353
QY	390	IRREVTDBDTRHLSRKFWDWAYGVPYSSLYDLSSLDTCGEASVLEILVY-NSKIENRHE	448

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Db      354 LQREIQEPECHLSRKFTWAYGPHSSLYDLSCIDTC-EKNSVLEVIAYSSSETPNRHD 412
Qy      449 MIAVEPIINELLADKRWKFGAVSYINVSYLCAVIFLTAYOQPLEGTPPYPTTVDY 508
Db      413 MLLVEPLNRLLODKWDRFVKRIFFENFLVCLYMIIFTMAAYRPRVDGLPPFKMEKTGDY 472
Qy      509 LRLAGEVITLFTGVLFVFFFTNIDLFMKKCPGVNSLFDGSPQLLYFIYSVLVISAALYL 568
Db      473 FRVTGEILSVLGGVFFFRGQI-Q-YLQRRPSSMKTLPVDSYSEMLFFLQSLFMLATVLYF 531
Qy      569 AGIEAYLAVMVFALVGLWMNALYFTRGKLTCTYSIMIKILFKDLFRFLVYLLFMIGY 628
Db      532 SHLKEYVASWVFSALGWTNMLYTRGQOMGIYAVMIEKMLRLDLCRFMFVYVFLFGF 591
Qy      629 ASALVSLNPNCANMKVCNEDQTNCTVPTY-----PSCRDSET-----FSTFLDLDFK 675
Db      592 STAVVTLI-----EDGKNDLSPESTSHRWGPACRPPDSSVNSLYST-CLELFFK 640
Qy      676 LTIGMGDLEMLSSTKYPVVFIILLVYIILTFVILLNMLIALMGSETVGVSKESHIWKL 735
Db      641 FTIGMGDLFTENYDFKAVFIILLAYVILLYILLNMLIALMGSETVKNIAQESKNIWKL 700
Qy      736 Q 736
Db      701 Q 701

RESULT 12
US-09-235-451-34
; Sequence 34, Application US/09235451
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 9076/084CIP
; CURRENT APPLICATION NUMBER: US/09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-235-451-34

Query Match 40.3%; Score 1556.5; DB 3; Length 839;
Best Local Similarity 44.5%; Pred. No. 5.1e-139;
Matches 321; Conservative 138; Mismatches 188; Indels 74; Gaps 12;

Qy      49 PSPADASRPAGCGDRPNL-----RMKFGQ-----AFKGVNPNIDLES--TLYESSV 95
Db      22 PDPLDGDPSRPPPAKPOLSTAKSRTRLFKGDSEEPVDCPHEEGELDCPTITVSPV 81
Qy      96 V-----PGPKKAPMDSLFDYGTGRHSSDNKRWRKIIERKQSPKAPAPQPPPIKLVF 149
Db      82 ITIQPGDGPPTGARL-----LSQDSVAASTEKTLRLY 113
Qy      150 NRPILFDIVSRGSTADLGLLPFLTHKKRLTDBEFREPSGTGKCLPKALINLNGRNDT 209
Db      114 DRRSIFEVAQNQCQDLESLLFLQSKKHLTDNEFKDPETGKCTCLKAMLNLDGQWTT 173
Qy      210 IPIVLLDIAERTGNMREFNSPRDIYRGQATLHAIATERRCKHYVELLVAQADVHAQAR 269
Db      174 IPIVLLDIAERTQDSLKELVNASYTSYKGTQATLHAIATERRNVALVTLLEVAGADVQAHAH 233

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Qy      270 GRFQPKDEGGYFVFGELPLSLAACTNOPHIVNLTENPHKKADMRRODSRGNTVLHALV 329
Db      234 GDFFKTKYRGCGTFGELPLSLAACTNQLGIVKFLQLQNSWQTADISARDSVGNTVLHALV 293
Qy      330 AIADNTRNTKFTVMKYDLLLLKCARLPDPSNLENLAVLNNDGLSLPLMMAAKTGKIGIFOHI 389
Db      294 EVAQNTADNTKFTVSMYNEIILGAKLHPTLKEELTNKKGMTPLAAGTGKIGVLAYI 353
Qy      390 IRREVTDEDTHLRKRKFKDWAYGPHYVSYSLYDLSSLDTCGEASVLEILVY-NSKIENRHE 448
Db      354 LQREIQEPECHLSRKFTWAYGPHSSLYDLSCIDTC-EKNSVLEVIAYSSSETPNRHD 412
Qy      449 MIAVEPIINELLADKRWKFGAVSYINVSYLCAVIFLTAYOQPLEGTPPYPTTVDY 508
Db      413 MLLVEPLNRLLODKWDRFVKRIFFENFLVCLYMIIFTMAAYRPRVDGLPPFKMEKTGDY 472
Qy      509 LRLAGEVITLFTGVLFVFFFTNIDLFMKKCPGVNSLFDGSPQLLYFIYSVLVISAALYL 568
Db      473 FRVTGEILSVLGGVFFFRGQI-Q-YLQRRPSSMKTLPVDSYSEMLFFLQSLFMLATVLYF 531
Qy      569 AGIEAYLAVMVFALVGLWMNALYFTRGKLTCTYSIMIKILFKDLFRFLVYLLFMIGY 628
Db      532 SHLKEYVASWVFSALGWTNMLYTRGQOMGIYAVMIEKMLRLDLCRFMFVYVFLFGF 591
Qy      629 ASALVSLNPNCANMKVCNEDQTNCTVPTY-----PSCRDSET-----FSTFLDLDFK 675
Db      592 STAVVTLI-----EDGKNDLSPESTSHRWGPACRPPDSSVNSLYST-CLELFFK 640
Qy      676 LTIGMGDLEMLSSTKYPVVFIILLVYIILTFVILLNMLIALMGSETVGVSKESHIWKL 735
Db      641 FTIGMGDLFTENYDFKAVFIILLAYVILLYILLNMLIALMGSETVKNIAQESKNIWKL 700
Qy      736 Q 736
Db      701 Q 701

RESULT 13
US-09-978-303-34
; Sequence 34, Application US/09978303
; Patent No. 6790629
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: Nucleic acid sequences encoding
; TITLE OF INVENTION: capsaicin receptor and capsaicin receptor-related
; TITLE OF INVENTION: polypeptides and uses thereof
; FILE REFERENCE: UCAL084CON
; CURRENT APPLICATION NUMBER: US/09/978,303
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-303-34

Query Match 40.3%; Score 1556.5; DB 4; Length 839;
Best Local Similarity 44.5%; Pred. No. 5.1e-139;
Matches 321; Conservative 138; Mismatches 188; Indels 74; Gaps 12;

Qy      49 PSPADASRPAGCGDRPNL-----RMKFGQ-----AFKGVNPNIDLES--TLYESSV 95
Db      22 PDPLDGDPSRPPPAKPOLSTAKSRTRLFKGDSEEPVDCPHEEGELDCPTITVSPV 81

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82 I:IORPGDGGTGARL-----LSQDSVAASTEXTLRY 113
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150 NRPTLFDIVSRGSGTADLDGLPELLTHKKRLTDBEFREPSGTCKTCLPKALLNLSNGRNDT 209
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    :||:
114 DRRSIFAVAOQNCODLESLLFLQSKKHITDNEFKDPETGKTCLLKAMLNHLHGQNTT 173
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210 IPVLLDIAERTGNMREPSFRDIYRGQTALHIAIERRCKHYVELLVAOADVHAQAR 269
    :||:
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174 IPLLLELARTQDSLKELVNASYTSYKQGTALHIAIERNNALVTLVLVENGADVQAAAH 233
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270 GRFPQKDEGGYFYFGBLPLSLAECTNOPHIVNYLTENPHKKADMRRDORSGNTVLHALV 329
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234 GDFPKTKGRPGFYFGBLPLSLAECTNQLGIVKFLQNSWTADISARDSVGNTVLHALV 293
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330 AIADNTENTKFTVMYDLLLLKCARLPDPSNLEAVTNNDGLSPLMMAAKTGKIGIPOHI 389
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294 EVADNTADNTKFTVSMYNEIILGAKLHPTLKLBELTNKKGMTPLALAAGTGKIGVLAYI 353
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390 IRREVTDDETHLSRKPDMWAYGPVSSLYDLSSLDTGEBASVLEILVY-NSKTIENRHE 448
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354 LQRIEQIPECKHLGRKFTWAYGPVHSSLYDLSDCTDC-EKNSVLEVIATVSSETPNRHD 412
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449 MLAVEPINELLRDKWRKFGAVSFYNVVSYLCAWVIFLTAYIQPLEGTPPYPTTVDY 508
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413 MLLAVEPLNRLLODKWRDVRKRIFFYNFLVYCLYMIIFTMAAYYRPVDOGLPFPKMEKTGY 472
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509 LRLAGEVITLTPGVLFPTNTIKDLPMMKCPGVNSLFDIGSGFQLLYFYISVLVIVSAALYL 568
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473 FRVTGEILSVLGGVYFFPRGIQ-YFLQRRPSNMKTLFVDSYSEMLFFLOSLFLMATWLYF 531
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569 AGIEAYLAVMVFALVLGWMNALYTRGLKLGTYSIMIOKILFKDLFRFLLVYLLFMICY 628
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532 SHLKEYASVMVFSLALGWTNNLYYTRGQOMGIYAVMIETKMILRDLCRFMFYVYVFLFEG 591
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676 LTIWGDLEMLSSTKYPVVFVILVYITLFTVLLNNMLIALMGSTVGQVSKESKHVKL 735
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641 FTICMGDLEFTENYDFRAVFILLAYVILTYLLNNMLIALMGSTVKNIAQESKNVKL 700
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736 Q 736
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701 Q 701

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RESULT 14
US-09-533-220A-2
; Sequence 2, Application US/09533220A
; Patent No. 6406908
; GENERAL INFORMATION:
; APPLICANT: McIntyre, Peter
; APPLICANT: James, Iain Fraser
; TITLE OF INVENTION: Human Vanilloid Receptor
; FILE REFERENCE: 4-30875A
; CURRENT APPLICATION NUMBER: US/09/533,220A
; CURRENT FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: UNITED KINGDOM 9907097.1
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 1.30
; SEQ ID NO 2
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-533-220A-2

Query Match	40.3%	Score 1555.5;	DB 4;	Length 839;
Best Local Similarity	44.5%	Pred. No. 6.4e-139;		
Matches 321;	Conservative 137;	Mismatches 189;	Indels 74;	Gaps 12;

RESULT 15
US-09-949-016-6937
Sequence 6937, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CUG001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0


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; SEQ ID NO 6937
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6937

Query Match      40.3%; Score 1555.5; DB 4; Length 839;
Best Local Similarity 44.5%; Pred. No. 6.4e-139;
Matches 321; Conservative 137; Mismatches 189; Indels 74; Gaps 12;

QY 49 PSPADASRPAAGDGRPNJ-----RMKFG-----AFKGVNPIDILLES--TLYESSV 95
Db 22 PDPLDGDNSRPPPAKPOLSTAKSTRFLRGKGDSEAFVDCPHEGELDCPTITVSPV 81
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QY 150 NRPIILDIVSRGSTADLDGLLPFLILTHKKRLTDEFEFREPSTGKTCCLKALLNLNNGRNDT 209
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QY 210 IPIVLIDIAERTGNMREFINSFRDIYRGQTALHIAIERCKHYVELLVAGADVHAQAR 269
Db 174 IPLLLEIARQTDLSKELVNASYTDSYRGQTALHIAIERNNMALVTLLVENGADVQAAAH 233
QY 270 GRFFQPKDEGGVYFGEPLSLAACTNQPHIVNLTENPHKKADMRRDSSRGNTVLHALV 329
Db 234 GDFFKTKGRPGFYFGEPLSLAACTNQGLIVKFLQNSWOTADISARDSVGNVTVLHALV 293
QY 330 AIADNTRENTKFTVTKYDLLLLKCARLPFSDNLEAVLNNDGLSLPLMMAAKTKIGIFQHI 389
Db 294 EVAADNTADNTKFTVSMYNEIILGAKLHPTLKEELTNKKGWPLAALAAAGTKIGVLAYI 353
QY 390 IRREVTDDETRHLSRKFKDMAYGPVYSSLYDLSSLDTCGEASVLEILVY-NSKIENRHE 448
Db 354 LQREIQEPECEHLSRKFTWAYGPHVSSLYDLSCIDTC-EKNSVLEVIAYSSSETPNRHD 412
QY 449 MIAVEPINELLARDKWRKFGAVSFYINVSYLCAWVIFTLTAYOPLGCTPPYPTTVDY 508
Db 413 MLLVEPLNRLIQDKWRDFVKRIFYNFLVLYCLYMIIFTMAAYRYPVDGLPPFKMEKTGDY 472
QY 509 LRLAGEVITLFTGVLFPTNIKDLFMKCPGVNSLFDGSPQLLYFYISVLVIVSAAIYL 568
Db 473 FRVTGEILSVLGVVYFFRGIQ-YFLQRRPSMKTFLVDSYSEMLFFLQSLFMLATVVLYF 531
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QY 736 Q 736
Db 701 Q 701
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Search completed: May 4, 2005, 22:24:40
Job time : 47 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 22:15:29 ; Search time 140 Seconds
(without alignments)
1765.463 Million cell updates/sec

Title: US-10-090-215-12

Perfect score: 3858

Sequence: 1 MADSEGRAGGVEAELPG.....GVSKESKHIWKLQSGRRRL 742

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:**

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3858	100.0	742	14	US-10-090-215-12
2	3858	100.0	742	17	US-10-090-215-12
3	3829	99.2	831	15	US-10-342-844-76
4	3829	99.2	870	16	US-10-761-085-2
5	3829	99.2	871	10	US-09-870-090-2
6	3829	99.2	871	14	US-10-000-823-7
7	3829	99.2	871	14	US-10-171-319-17
8	3829	99.2	871	15	US-10-342-844-58
9	3829	99.2	871	15	US-10-342-844-58
10	3829	99.2	871	15	US-10-342-844-78
11	3829	99.2	871	16	US-10-415-570A-2
12	3828	99.2	871	14	US-10-027-828-2
13	3828	99.2	871	15	US-10-342-844-60

14	3825	99.1	871	14	US-10-027-828-4	Sequence 4, Appli
15	3823	99.1	871	14	US-10-090-215-7	Sequence 7, Appli
16	3823	99.1	871	17	US-10-985-156-7	Sequence 7, Appli
17	3810	98.8	963	10	US-09-932-165-1477	Sequence 1477, Ap
18	3809	98.7	871	14	US-10-227-255A-3	Sequence 3, Appli
19	3695	95.8	871	15	US-10-342-844-84	Sequence 84, Appli
20	3693	95.7	830	14	US-10-027-828-6	Sequence 6, Appli
21	3693	95.7	871	14	US-10-027-828-11	Sequence 11, Appli
22	3693	95.7	871	15	US-10-342-844-66	Sequence 66, Appli
23	3689	95.6	871	15	US-10-342-844-80	Sequence 80, Appli
24	3687	95.6	871	14	US-10-027-828-10	Sequence 10, Appli
25	3686	95.5	871	14	US-10-027-828-8	Sequence 8, Appli
26	3686	95.5	871	14	US-10-027-828-9	Sequence 9, Appli
27	3685	95.5	871	14	US-10-171-319-14	Sequence 14, Appli
28	3681	95.4	871	14	US-10-227-255A-1	Sequence 1, Appli
29	3652	94.7	870	14	US-10-027-828-13	Sequence 13, Appli
30	3636	94.2	873	15	US-10-342-844-64	Sequence 64, Appli
31	3472	90.0	803	15	US-10-342-844-56	Sequence 56, Appli
32	3470	89.9	811	14	US-10-090-215-9	Sequence 9, Appli
33	3470	89.9	811	17	US-10-985-156-9	Sequence 9, Appli
34	3467	89.9	792	9	US-09-764-367A-2	Sequence 2, Appli
35	3457	89.6	803	9	US-09-764-367A-8	Sequence 8, Appli
36	3389	87.8	803	15	US-10-342-844-62	Sequence 62, Appli
37	3284	85.1	852	14	US-10-027-828-15	Sequence 15, Appli
38	3284	85.1	852	15	US-10-342-844-36	Sequence 36, Appli
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40	3044.5	78.9	734	9	US-09-764-367A-4	Sequence 4, Appli
41	2847	73.8	625	10	US-09-932-165-1507	Sequence 1507, Ap
42	2782	72.1	625	10	US-09-932-165-1506	Sequence 1506, Ap
43	2373.5	61.5	602	10	US-09-870-090-4	Sequence 4, Appli
44	2373.5	61.5	602	16	US-10-761-065-4	Sequence 4, Appli
45	2156.5	55.9	559	15	US-10-297-022-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-10-090-215-12
; Sequence 12, Application US/10090215
; Publication No. US20030032097A1
; GENERAL INFORMATION:
; APPLICANT: Dublin, Adrienne E
; APPLICANT: Huvar, Arne
; APPLICANT: Erlander, Mark G
; APPLICANT: Glass, Charles A
; TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor
; TITLE OF INVENTION: VR3
; FILE REFERENCE: Human VR3 receptors
; CURRENT APPLICATION NUMBER: US/10/090,215
; CURRENT FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 12
; LENGTH: 742
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-090-215-12

Query Match 100.0%; Score 3858; DB 14; Length 742;
Best Local Similarity 100.0%; Pred. No. 9.8e-308;
Matches 742; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MADSEGRAGGVEAELPGDESGTGGGEAFPLSLANLFEGEDGSLSPSPADASRPAGP 60
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DB 61 GDGRNLRMKFGCAFKGVNPIDILLESYESSVVPGPKAPMDSLFDYGYRHHSSDN 120
QY 121 KWRKRIIEKQPSKAPAPQPPPIKVFNPRIIFDIVSRGSTADLDGLLPFLTHKKKL 180

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Db 121 KRWKKIIEKQPSKAPAPQPPILKVFNRPILFDIVSRGSTADLDGLLFPLLTHKKRL 180
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Db 181 TDEEFPREPSTGKTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOT 240
Qy 241 ALHIAIERRCKHYVELLVAQADVHAQARGFPQPKDEGGYFYFGEPLSLAACTNQPHI 300
Db 241 ALHIAIERRCKHYVELLVAQADVHAQARGFPQPKDEGGYFYFGEPLSLAACTNQPHI 300
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Db 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKLCARLPDS 360
Qy 361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDETRHLSRKFKDWAYGVPVSSLYD 420
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Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYINVSYLE 480
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Qy 601 TYSIMIQLFKDLFRFLLVLLFMIGVASALVSLNPNCAVMKVCNEDQTNCTVPTPSC 660
Db 601 TYSIMIQLFKDLFRFLLVLLFMIGVASALVSLNPNCAVMKVCNEDQTNCTVPTPSC 660
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Db 661 RDSEFTSFLLDLFKLTIGMGDLEMLSTKYPVVFIIILVTYIILTFVLLNMLIALMGE 720
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Db 721 TVGVSKESKHIWKLOSGRRRL 742
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RESULT 2

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; Sequence 12, Application US/10985156
; Publication No. US20050084897A1
; GENERAL INFORMATION:
; APPLICANT: Dubin, Adrienne E
; APPLICANT: Huvar, Arne
; APPLICANT: Erlanger, Mark G
; APPLICANT: Glass, Charles A
; TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor
; FILE REFERENCE: Human VR3 receptors
; CURRENT APPLICATION NUMBER: US/10/985,156
; PRIOR FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/10/090,215
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 742
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-985-156-12
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Query Match 100.0%; Score 3858; DB 17; Length 742;
Best Local Similarity 100.0%; Pred. No. 9.8e-308;
Matches 742; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MADSEGPAGPGEVAELPGDESGTGPCGEAPFLSSLANLFEDEGSLSPSPADASRRPAGP 60
Qy 61 GDGRPNLRMKFQGAFRKGVNPNPIDLLESTLYESSVVPGPKKAPMDSLFYGYTRHSSDN 120
Db 61 GDGRPNLRMKFQGAFRKGVNPNPIDLLESTLYESSVVPGPKKAPMDSLFYGYTRHSSDN 120
Qy 121 KRWKKIIEKQPSKAPAPQPPILKVFNRPILFDIVSRGSTADLDGLLFPLLTHKKRL 180
Db 121 KRWKKIIEKQPSKAPAPQPPILKVFNRPILFDIVSRGSTADLDGLLFPLLTHKKRL 180
Qy 181 TDEEFPREPSTGKTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOT 240
Db 181 TDEEFPREPSTGKTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOT 240
Qy 241 ALHIAIERRCKHYVELLVAQADVHAQARGFPQPKDEGGYFYFGEPLSLAACTNQPHI 300
Db 241 ALHIAIERRCKHYVELLVAQADVHAQARGFPQPKDEGGYFYFGEPLSLAACTNQPHI 300
Qy 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKLCARLPDS 360
Db 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKLCARLPDS 360
Qy 361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDETRHLSRKFKDWAYGVPVSSLYD 420
Db 361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDETRHLSRKFKDWAYGVPVSSLYD 420
Qy 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYINVSYLE 480
Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYINVSYLE 480
Qy 481 AMVIFTLTAYTQPLEGTPPYRTTVDYLRAGEVITLFTGVLFEEFTNIKDLFMKKCPGV 540
Db 481 AMVIFTLTAYTQPLEGTPPYRTTVDYLRAGEVITLFTGVLFEEFTNIKDLFMKKCPGV 540
Qy 541 NSLFDGSGFOLLFYIYSVLIVSAALYAGIAYLAVNVFALVIGWNNALYFTRGKLTG 600
Db 541 NSLFDGSGFOLLFYIYSVLIVSAALYAGIAYLAVNVFALVIGWNNALYFTRGKLTG 600
Qy 601 TYSIMIQLFKDLFRFLLVLLFMIGVASALVSLNPNCAVMKVCNEDQTNCTVPTPSC 660
Db 601 TYSIMIQLFKDLFRFLLVLLFMIGVASALVSLNPNCAVMKVCNEDQTNCTVPTPSC 660
Qy 661 RDSEFTSFLLDLFKLTIGMGDLEMLSTKYPVVFIIILVTYIILTFVLLNMLIALMGE 720
Db 661 RDSEFTSFLLDLFKLTIGMGDLEMLSTKYPVVFIIILVTYIILTFVLLNMLIALMGE 720
Qy 721 TVGVSKESKHIWKLOSGRRRL 742
Db 721 TVGVSKESKHIWKLOSGRRRL 742
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RESULT 3

```
US-10-342-844-76
; Sequence 76, Application US/10342844
; Publication No. US20040009537A1
; GENERAL INFORMATION:
; APPLICANT: Roos, Jack
; APPLICANT: Stauderman, Kenneth
; APPLICANT: Velicelebi, G'n I
; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
; TITLE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCIUM
; FILE REFERENCE: 37481-3307
; CURRENT APPLICATION NUMBER: US/10/342,844
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/347,459
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/401,171
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/405,678
; PRIOR FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76
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; LENGTH: 831
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 804, 816
; OTHER INFORMATION: Xaa = Any Amino Acid
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank XP_012261
; DATABASE ENTRY DATE: 2001-10-16
US-10-342-844-76

Query Match      99.2%; Score 3829; DB 15; Length 831;
Best Local Similarity 100.0%; Pred. No. 2.8e-305;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSEGPAGGGEVAELPGDESGTGGGEAPLSSLANLFEGEDGSLSPSPADASRPAGP 60
DB 1 MADSEGPAGGGEVAELPGDESGTGGGEAPLSSLANLFEGEDGSLSPSPADASRPAGP 60

QY 61 GDGRNLRMKFOGAFKGVNPNIDLESTLYESSVVPKAPMDSLPDYGYRHHSSDN 120
DB 61 GDGRNLRMKFOGAFKGVNPNIDLESTLYESSVVPKAPMDSLPDYGYRHHSSDN 120

QY 121 KWRKKIIEKQSPKAPAPQPPILKVFNRPILEDIVSRGSTADLDGLLPFLTHKKRL 180
DB 121 KWRKKIIEKQSPKAPAPQPPILKVFNRPILEDIVSRGSTADLDGLLPFLTHKKRL 180

QY 181 TDEEPRESTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGQT 240
DB 181 TDEEPRESTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGQT 240

QY 241 ALHIAIERCKHYVELLVAQADVHAQARGFPQPKDEGGYFYFGELPLSLAACTNQPHI 300
DB 241 ALHIAIERCKHYVELLVAQADVHAQARGFPQPKDEGGYFYFGELPLSLAACTNQPHI 300

QY 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDLLLLKCARLPDPS 360
DB 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDLLLLKCARLPDPS 360

QY 361 NLEAVLNNDGLSPLMAAATKGIGIFQHIIRREVTDTRHLRSRKFQKWAYGVPVYSSLYD 420
DB 361 NLEAVLNNDGLSPLMAAATKGIGIFQHIIRREVTDTRHLRSRKFQKWAYGVPVYSSLYD 420

QY 421 LSSLTCCGEASVLEILVYNSKIENRHEMLAVEPINEILLRDKWRKFGAVSFYINVVSYLEC 480
DB 421 LSSLTCCGEASVLEILVYNSKIENRHEMLAVEPINEILLRDKWRKFGAVSFYINVVSYLEC 480

QY 481 AMVIFTLTAYQPLEGTPPYVRTTVDYLRLAGEVITLFTGVLFFFTNIKOLFMMKKCPGV 540
DB 481 AMVIFTLTAYQPLEGTPPYVRTTVDYLRLAGEVITLFTGVLFFFTNIKOLFMMKKCPGV 540

QY 541 NSLFDGSGQLLYFYYSVLVIVSAALYLAGIBAYLAVMVVFLVGLWMNALYFTRGLKLTG 600
DB 541 NSLFDGSGQLLYFYYSVLVIVSAALYLAGIBAYLAVMVVFLVGLWMNALYFTRGLKLTG 600

QY 601 TVSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQCTVPTPSC 660
DB 601 TVSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQCTVPTPSC 660

QY 661 RDSETFSTFLDLFKLTIGMGDLEMLSSTKYPVWFILLVTVIILTFVLLANMLALMGE 720
DB 661 RDSETFSTFLDLFKLTIGMGDLEMLSSTKYPVWFILLVTVIILTFVLLANMLALMGE 720

QY 721 TVGQVSKESKHIWKQLQ 736
DB 721 TVGQVSKESKHIWKQLQ 736
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RESULT 4

```
US-10-761-065-2
; Sequence 2, Application US/10761065
; Publication No. US20040137573A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; APPLICANT: Katsuhiko Shinjo
; APPLICANT: Hikaru Yabuuchi
; TITLE OF INVENTION: Human Vanilloid Receptor-Like Proteins
; FILE REFERENCE: PC9979ADAM
; CURRENT APPLICATION NUMBER: US/10/761,065
; CURRENT FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US/09/870,090A
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: US 60/208,156
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 870
; TYPE: PRT
; ORGANISM: Human
US-10-761-065-2
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Query Match      99.2%; Score 3829; DB 16; Length 870;
Best Local Similarity 100.0%; Pred. No. 3e-305;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSEGPAGGGEVAELPGDESGTGGGEAPLSSLANLFEGEDGSLSPSPADASRPAGP 60
DB 1 MADSEGPAGGGEVAELPGDESGTGGGEAPLSSLANLFEGEDGSLSPSPADASRPAGP 60

QY 61 GDGRNLRMKFOGAFKGVNPNIDLESTLYESSVVPKAPMDSLPDYGYRHHSSDN 120
DB 61 GDGRNLRMKFOGAFKGVNPNIDLESTLYESSVVPKAPMDSLPDYGYRHHSSDN 120

QY 121 KWRKKIIEKQSPKAPAPQPPILKVFNRPILEDIVSRGSTADLDGLLPFLTHKKRL 180
DB 121 KWRKKIIEKQSPKAPAPQPPILKVFNRPILEDIVSRGSTADLDGLLPFLTHKKRL 180

QY 181 TDEEPRESTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGQT 240
DB 181 TDEEPRESTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGQT 240

QY 241 ALHIAIERCKHYVELLVAQADVHAQARGFPQPKDEGGYFYFGELPLSLAACTNQPHI 300
DB 241 ALHIAIERCKHYVELLVAQADVHAQARGFPQPKDEGGYFYFGELPLSLAACTNQPHI 300

QY 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDLLLLKCARLPDPS 360
DB 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDLLLLKCARLPDPS 360

QY 361 NLEAVLNNDGLSPLMAAATKGIGIFQHIIRREVTDTRHLRSRKFQKWAYGVPVYSSLYD 420
DB 361 NLEAVLNNDGLSPLMAAATKGIGIFQHIIRREVTDTRHLRSRKFQKWAYGVPVYSSLYD 420

QY 421 LSSLTCCGEASVLEILVYNSKIENRHEMLAVEPINEILLRDKWRKFGAVSFYINVVSYLEC 480
DB 421 LSSLTCCGEASVLEILVYNSKIENRHEMLAVEPINEILLRDKWRKFGAVSFYINVVSYLEC 480

QY 481 AMVIFTLTAYQPLEGTPPYVRTTVDYLRLAGEVITLFTGVLFFFTNIKOLFMMKKCPGV 540
DB 481 AMVIFTLTAYQPLEGTPPYVRTTVDYLRLAGEVITLFTGVLFFFTNIKOLFMMKKCPGV 540

QY 541 NSLFDGSGQLLYFYYSVLVIVSAALYLAGIBAYLAVMVVFLVGLWMNALYFTRGLKLTG 600
DB 541 NSLFDGSGQLLYFYYSVLVIVSAALYLAGIBAYLAVMVVFLVGLWMNALYFTRGLKLTG 600

QY 601 TVSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQCTVPTPSC 660
DB 601 TVSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPCANMKVCNEDQCTVPTPSC 660

QY 661 RDSETFSTFLDLFKLTIGMGDLEMLSSTKYPVWFILLVTVIILTFVLLANMLALMGE 720
DB 661 RDSETFSTFLDLFKLTIGMGDLEMLSSTKYPVWFILLVTVIILTFVLLANMLALMGE 720

QY 721 TVGQVSKESKHIWKQLQ 736
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Db 721 TVGQVSKESKHIWKIQ 736
|||||

RESULT 5

US-09-870-090-2
; Sequence 2, Application US/09870090
; Publication No. US20030017527A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Product Inc.
; TITLE OF INVENTION: Human Vanilloid Receptor-Like Proteins
; FILE REFERENCE: PC9979A
; CURRENT APPLICATION NUMBER: US/09/870,090
; CURRENT FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: US 60/208,156
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Human
US-09-870-090-2

Query Match 99.2%; Score 3829; DB 10; Length 871;
Best Local Similarity 100.0%; Pred. No. 3e-305;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSEGPAGGGEVAELPGDESGTPGGEAFPLSSLANLFEDEGSLSPSPADASRRPAGP 60
Db 1 MADSEGPAGGGEVAELPGDESGTPGGEAFPLSSLANLFEDEGSLSPSPADASRRPAGP 60

QY 61 GDGRNLRMKFQAGRKGVNPNIDLLSTLYESSVVPQPKAPMDSLFDYGTYYRHSSDN 120
Db 61 GDGRNLRMKFQAGRKGVNPNIDLLSTLYESSVVPQPKAPMDSLFDYGTYYRHSSDN 120

QY 121 KRWKKKIIEKQPSKAPAPOPPPILKVFNRPILFDIVSRGSTADLDGLLPFLTHKKRL 180
Db 121 KRWKKKIIEKQPSKAPAPOPPPILKVFNRPILFDIVSRGSTADLDGLLPFLTHKKRL 180

QY 181 TDEFPREPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGQT 240
Db 181 TDEFPREPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGQT 240

QY 241 ALHTAIERRCKHYVELLVAQADVHAQARGFFQPKDEGGYFYFGEPLSLAACTNQPHI 300
Db 241 ALHTAIERRCKHYVELLVAQADVHAQARGFFQPKDEGGYFYFGEPLSLAACTNQPHI 300

QY 301 VNYLTENPHKKADMRQDSRGNTVLAHALVAIDNTRENTKFTVMYDLLLLKCARLPFDS 360
Db 301 VNYLTENPHKKADMRQDSRGNTVLAHALVAIDNTRENTKFTVMYDLLLLKCARLPFDS 360

QY 361 NLEAVLNNDGLSPLMAAATKIGIFQHIIRREVTDTRHLSRKFKDWAYGPPVSSLYD 420
Db 361 NLEAVLNNDGLSPLMAAATKIGIFQHIIRREVTDTRHLSRKFKDWAYGPPVSSLYD 420

QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKRWKFGAVSVINVSYLE 480
Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKRWKFGAVSVINVSYLE 480

QY 481 AMVIFTLTAYTQPLEGTPPYRTTVDYLRAGEVITLFTGVLPFFFTNIKDLFMKKCPGV 540
Db 481 AMVIFTLTAYTQPLEGTPPYRTTVDYLRAGEVITLFTGVLPFFFTNIKDLFMKKCPGV 540

QY 541 NSLFDIGSFQLLYFTYSVLVVSAAALVLAGIEAYLVNMFALVGMNALLYFTTGLKLTG 600
Db 541 NSLFDIGSFQLLYFTYSVLVVSAAALVLAGIEAYLVNMFALVGMNALLYFTTGLKLTG 600

QY 601 TYSIMIQILKDLFRLLVLLFMVGYASALVSLNFCANNKVCNEDQTNCTVTPYPS 660
Db 601 TYSIMIQILKDLFRLLVLLFMVGYASALVSLNFCANNKVCNEDQTNCTVTPYPS 660

QY 661 RDSFTFSLDLFLKLTIGMGDLEMLSSTKYPVVFIIILLVTVIITFTVLLNMLIALMGE 720

Db 661 RDSFTFSLDLFLKLTIGMGDLEMLSSTKYPVVFIIILLVTVIITFTVLLNMLIALMGE 720
QY 721 TVGQVSKESKHIWKIQ 736
Db 721 TVGQVSKESKHIWKIQ 736
|||||

RESULT 6

US-10-000-823-7
; Sequence 7, Application US/10000823
; Publication No. US20030027164A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING A NOVEL HUMAN ION CHANNEL EXPRESSED IN SPINAL CORD AND BRAIN
; FILE REFERENCE: D0109NP
; CURRENT APPLICATION NUMBER: US/10/000,823
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/250,587
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-823-7

Query Match 99.2%; Score 3829; DB 14; Length 871;
Best Local Similarity 100.0%; Pred. No. 3e-305;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSEGPAGGGEVAELPGDESGTPGGEAFPLSSLANLFEDEGSLSPSPADASRRPAGP 60
Db 1 MADSEGPAGGGEVAELPGDESGTPGGEAFPLSSLANLFEDEGSLSPSPADASRRPAGP 60

QY 61 GDGRNLRMKFQAGRKGVNPNIDLLSTLYESSVVPQPKAPMDSLFDYGTYYRHSSDN 120
Db 61 GDGRNLRMKFQAGRKGVNPNIDLLSTLYESSVVPQPKAPMDSLFDYGTYYRHSSDN 120

QY 121 KRWKKKIIEKQPSKAPAPOPPPILKVFNRPILFDIVSRGSTADLDGLLPFLTHKKRL 180
Db 121 KRWKKKIIEKQPSKAPAPOPPPILKVFNRPILFDIVSRGSTADLDGLLPFLTHKKRL 180

QY 181 TDEFPREPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGQT 240
Db 181 TDEFPREPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGQT 240

QY 241 ALHTAIERRCKHYVELLVAQADVHAQARGFFQPKDEGGYFYFGEPLSLAACTNQPHI 300
Db 241 ALHTAIERRCKHYVELLVAQADVHAQARGFFQPKDEGGYFYFGEPLSLAACTNQPHI 300

QY 301 VNYLTENPHKKADMRQDSRGNTVLAHALVAIDNTRENTKFTVMYDLLLLKCARLPFDS 360
Db 301 VNYLTENPHKKADMRQDSRGNTVLAHALVAIDNTRENTKFTVMYDLLLLKCARLPFDS 360

QY 361 NLEAVLNNDGLSPLMAAATKIGIFQHIIRREVTDTRHLSRKFKDWAYGPPVSSLYD 420
Db 361 NLEAVLNNDGLSPLMAAATKIGIFQHIIRREVTDTRHLSRKFKDWAYGPPVSSLYD 420

QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKRWKFGAVSVINVSYLE 480
Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKRWKFGAVSVINVSYLE 480

QY 481 AMVIFTLTAYTQPLEGTPPYRTTVDYLRAGEVITLFTGVLPFFFTNIKDLFMKKCPGV 540
Db 481 AMVIFTLTAYTQPLEGTPPYRTTVDYLRAGEVITLFTGVLPFFFTNIKDLFMKKCPGV 540

QY 541 NSLFDIGSFQLLYFTYSVLVVSAAALVLAGIEAYLVNMFALVGMNALLYFTTGLKLTG 600
Db 541 NSLFDIGSFQLLYFTYSVLVVSAAALVLAGIEAYLVNMFALVGMNALLYFTTGLKLTG 600

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QY 601 TYSIMQIKLFDLFRLLVLLFMIGYASALVSLNFCANNKVCNEQDQTNCTVPTPSC 660
DB 601 TYSIMQIKLFDLFRLLVLLFMIGYASALVSLNFCANNKVCNEQDQTNCTVPTPSC 660
QY 661 RDSFTSFLLDLFKLTGMDLMSLSTKYPVVFIIILLVYIILTFVLLNMLIALMGE 720
DB 661 RDSFTSFLLDLFKLTGMDLMSLSTKYPVVFIIILLVYIILTFVLLNMLIALMGE 720
QY 721 TVGQVSKESKHIWKLO 736
DB 721 TVGQVSKESKHIWKLO 736

RESULT 7
US-10-171-319-17
; Sequence 17, Application US/10171319
; Publication No. US20030157633A1
; GENERAL INFORMATION:
; APPLICANT: Ardem Patapoutian
; APPLICANT: Andrea Peier
; APPLICANT: Peter McIntyre
; APPLICANT: Stuart Bevan
; APPLICANT: Chuansheng Song
; APPLICANT: Pamposh Ganju
; TITLE OF INVENTION: VANILLOID RECEPTOR-RELATED NUCLEIC ACIDS
; TITLE OF INVENTION: AND POLYPEPTIDES
; FILE REFERENCE: 4-32048A
; CURRENT APPLICATION NUMBER: US/10/171,319
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/297,835
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: 60/351,238
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/352,914
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: 60/357,161
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/381,086
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/381,739
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-319-17

Query Match 99.2%; Score 3829; DB 14; Length 871;
Best Local Similarity 100.0%; Pred. No. 3e-305;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSEGPRAGGEVAELPGDESGTPGGEAPFLSSLANLFEGEDGSLSPSPADASRPAGP 60
DB 1 MADSSEGPRAGGEVAELPGDESGTPGGEAPFLSSLANLFEGEDGSLSPSPADASRPAGP 60
QY 61 GDGRNLRMKFGAFKRGVNPIDLLESTLYESSVVPKAPMDSLDYGYRHHSSDN 120
DB 61 GDGRNLRMKFGAFKRGVNPIDLLESTLYESSVVPKAPMDSLDYGYRHHSSDN 120
QY 121 KWRKKIIEKQPSKAPAPQPPILKVFNRPIILFDIVSRGSTADLDGLLPLLTHKKRL 180
DB 121 KWRKKIIEKQPSKAPAPQPPILKVFNRPIILFDIVSRGSTADLDGLLPLLTHKKRL 180
QY 181 TDEEFREPTGTCLPKALLNSGRNDTIPVLLDIAERTGNRRBFINSPPFDIYYRGOT 240
DB 181 TDEEFREPTGTCLPKALLNSGRNDTIPVLLDIAERTGNRRBFINSPPFDIYYRGOT 240
QY 241 ALHIAIERCKHYVELLVAQAGADVAHQARGRFPQPKDEGGYYPFGELPLSLAACTNQPHI 300
DB 241 ALHIAIERCKHYVELLVAQAGADVAHQARGRFPQPKDEGGYYPFGELPLSLAACTNQPHI 300
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QY 301 VNYLTENPHKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDLLLLLKCARLFPDS 360
DB 301 VNYLTENPHKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDLLLLLKCARLFPDS 360
QY 361 NLEAVLNNDGLSPLMAAKTKIGIFQHIIRREVTDDETRHLSRKFKDWAYGVPVYSSLYD 420
DB 361 NLEAVLNNDGLSPLMAAKTKIGIFQHIIRREVTDDETRHLSRKFKDWAYGVPVYSSLYD 420
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSILC 480
DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSILC 480
QY 481 AMVIFTLTAYYOPLGTPPYRTTVDYLRAGEVITLTFTGVLPFTTNIKOLFMMKKCPGV 540
DB 481 AMVIFTLTAYYOPLGTPPYRTTVDYLRAGEVITLTFTGVLPFTTNIKOLFMMKKCPGV 540
QY 541 NSLFDGSPQLLYFTYSVLVVSAAALYLAGIEAYLAVMVFAVLGMMNALYFTRGLKLTG 600
DB 541 NSLFDGSPQLLYFTYSVLVVSAAALYLAGIEAYLAVMVFAVLGMMNALYFTRGLKLTG 600
QY 601 TYSIMQIKLFDLFRLLVLLFMIGYASALVSLNFCANNKVCNEQDQTNCTVPTPSC 660
DB 601 TYSIMQIKLFDLFRLLVLLFMIGYASALVSLNFCANNKVCNEQDQTNCTVPTPSC 660
QY 661 RDSFTSFLLDLFKLTGMDLMSLSTKYPVVFIIILLVYIILTFVLLNMLIALMGE 720
DB 661 RDSFTSFLLDLFKLTGMDLMSLSTKYPVVFIIILLVYIILTFVLLNMLIALMGE 720
QY 721 TVGQVSKESKHIWKLO 736
DB 721 TVGQVSKESKHIWKLO 736

RESULT 8
US-10-342-844-54
; Sequence 54, Application US/10342844
; Publication No. US20040009537A1
; GENERAL INFORMATION:
; APPLICANT: Roos, Jack
; APPLICANT: Stauderman, Kenneth
; APPLICANT: Velicelebi, G'n'l
; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
; TITLE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCIUM
; FILE REFERENCE: 37481-3307
; CURRENT APPLICATION NUMBER: US/10/342,844
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/347,459
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/401,171
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/405,678
; PRIOR FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank XP_027181
; DATABASE ENTRY DATE: 2002-09-01
US-10-342-844-54

Query Match 99.2%; Score 3829; DB 15; Length 871;
Best Local Similarity 100.0%; Pred. No. 3e-305;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSEGPRAGGEVAELPGDESGTPGGEAPFLSSLANLFEGEDGSLSPSPADASRPAGP 60
DB 1 MADSSEGPRAGGEVAELPGDESGTPGGEAPFLSSLANLFEGEDGSLSPSPADASRPAGP 60
QY 61 GDGRNLRMKFGAFKRGVNPIDLLESTLYESSVVPKAPMDSLDYGYRHHSSDN 120
```

Db 61 GDGRPNLRMKFQAGFRKGVNPIDLLSTLYESSVVPKPKAPMDSLFDYGYRHHSSDN 120
QY 121 KWRKXKIIKQPOSQKAPAPQPPPIKVFNPILFDIVSRGSTDLDGLLFFLLTHKKRL 180
Db 121 KWRKXKIIKQPOSQKAPAPQPPPIKVFNPILFDIVSRGSTDLDGLLFFLLTHKKRL 180
QY 181 TDEFRPSTGKTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGQT 240
Db 181 TDEFRPSTGKTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGQT 240
QY 241 ALHIAIERCKHYVELLVAQAGDVHAQARGFRFPQKDEGGYFYFGEPLSLAACTNQPHI 300
Db 241 ALHIAIERCKHYVELLVAQAGDVHAQARGFRFPQKDEGGYFYFGEPLSLAACTNQPHI 300
QY 301 VNYLTENPHKADMRQDSRGNTVLHALVAADNTRENTKFTVMYDILLKCARLPDPS 360
Db 301 VNYLTENPHKADMRQDSRGNTVLHALVAADNTRENTKFTVMYDILLKCARLPDPS 360
QY 361 NLEAVLNDGLSPLMMAAKTGKIGIFQHIIRREVTDETRHLSRKFKDWAYGPVYSSLYD 420
Db 361 NLEAVLNDGLSPLMMAAKTGKIGIFQHIIRREVTDETRHLSRKFKDWAYGPVYSSLYD 420
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRKWKRFKGFVAVSVVSYLC 480
Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRKWKRFKGFVAVSVVSYLC 480
QY 481 AMVIFTLTAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
Db 481 AMVIFTLTAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
QY 541 NSLFIDGSQLLYFYISVIVSAALYLAGIAYLVAVMVFALVGMNLYFTRLKLTG 600
Db 541 NSLFIDGSQLLYFYISVIVSAALYLAGIAYLVAVMVFALVGMNLYFTRLKLTG 600
QY 601 TYSIMIQILFKDLFRLLVLLFMIGVASALVSLNPNCAKMKVCNEDQNTCTVPTPSC 660
Db 601 TYSIMIQILFKDLFRLLVLLFMIGVASALVSLNPNCAKMKVCNEDQNTCTVPTPSC 660
QY 661 RDSFTSFLLDLFKLTGMDLEMLSTKYPVVFIIILLVYIILTFVLLNMLIALMGE 720
Db 661 RDSFTSFLLDLFKLTGMDLEMLSTKYPVVFIIILLVYIILTFVLLNMLIALMGE 720
QY 721 TVGVQSKESKHIWKLO 736
Db 721 TVGVQSKESKHIWKLO 736

RESULT 9

US-10-342-844-58
; Sequence 58, Application US/10342844
; Publication No. US20040009537A1
; GENERAL INFORMATION:
; APPLICANT: Roos, Jack
; APPLICANT: Stauderman, Kenneth
; APPLICANT: Velicelebi, G'n 1
; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
; TITLE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCIUM
; FILE REFERENCE: 37481-3307
; CURRENT APPLICATION NUMBER: US/10/342,844
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/347,459
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/401,171
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/405,678
; PRIOR FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: Genbank BAB69040
; DATABASE ENTRY DATE: 2001-10-02
US-10-342-844-58

Query Match 99.2%; Score 3829; DB 15; Length 871;
Best Local Similarity 100.0%; Pred. No. 3e-305;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSEGPAGCGEVAELPGDESGTSGEAPPLSLANLFEDEGSLSPSPADASRRPAGP 60
Db 1 MADSEGPAGCGEVAELPGDESGTSGEAPPLSLANLFEDEGSLSPSPADASRRPAGP 60
QY 61 GDGRPNLRMKFQAGFRKGVNPIDLLSTLYESSVVPKPKAPMDSLFDYGYRHHSSDN 120
Db 61 GDGRPNLRMKFQAGFRKGVNPIDLLSTLYESSVVPKPKAPMDSLFDYGYRHHSSDN 120
QY 121 KWRKXKIIKQPOSQKAPAPQPPPIKVFNPILFDIVSRGSTDLDGLLFFLLTHKKRL 180
Db 121 KWRKXKIIKQPOSQKAPAPQPPPIKVFNPILFDIVSRGSTDLDGLLFFLLTHKKRL 180
QY 181 TDEFRPSTGKTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGQT 240
Db 181 TDEFRPSTGKTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGQT 240
QY 241 ALHIAIERCKHYVELLVAQAGDVHAQARGFRFPQKDEGGYFYFGEPLSLAACTNQPHI 300
Db 241 ALHIAIERCKHYVELLVAQAGDVHAQARGFRFPQKDEGGYFYFGEPLSLAACTNQPHI 300
QY 301 VNYLTENPHKADMRQDSRGNTVLHALVAADNTRENTKFTVMYDILLKCARLPDPS 360
Db 301 VNYLTENPHKADMRQDSRGNTVLHALVAADNTRENTKFTVMYDILLKCARLPDPS 360
QY 361 NLEAVLNDGLSPLMMAAKTGKIGIFQHIIRREVTDETRHLSRKFKDWAYGPVYSSLYD 420
Db 361 NLEAVLNDGLSPLMMAAKTGKIGIFQHIIRREVTDETRHLSRKFKDWAYGPVYSSLYD 420
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRKWKRFKGFVAVSVVSYLC 480
Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRKWKRFKGFVAVSVVSYLC 480
QY 481 AMVIFTLTAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
Db 481 AMVIFTLTAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
QY 541 NSLFIDGSQLLYFYISVIVSAALYLAGIAYLVAVMVFALVGMNLYFTRLKLTG 600
Db 541 NSLFIDGSQLLYFYISVIVSAALYLAGIAYLVAVMVFALVGMNLYFTRLKLTG 600
QY 601 TYSIMIQILFKDLFRLLVLLFMIGVASALVSLNPNCAKMKVCNEDQNTCTVPTPSC 660
Db 601 TYSIMIQILFKDLFRLLVLLFMIGVASALVSLNPNCAKMKVCNEDQNTCTVPTPSC 660
QY 661 RDSFTSFLLDLFKLTGMDLEMLSTKYPVVFIIILLVYIILTFVLLNMLIALMGE 720
Db 661 RDSFTSFLLDLFKLTGMDLEMLSTKYPVVFIIILLVYIILTFVLLNMLIALMGE 720
QY 721 TVGVQSKESKHIWKLO 736
Db 721 TVGVQSKESKHIWKLO 736

RESULT 10

US-10-342-844-78
; Sequence 78, Application US/10342844
; Publication No. US20040009537A1
; GENERAL INFORMATION:
; APPLICANT: Roos, Jack
; APPLICANT: Stauderman, Kenneth
; APPLICANT: Velicelebi, G'n 1
; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
; TITLE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCIUM
; FILE REFERENCE: 37481-3307
; CURRENT APPLICATION NUMBER: US/10/342,844


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; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/347,459
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/401,171
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/405,678
; PRIOR FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AAG16127
; DATABASE ENTRY DATE: 2000-09-26
US-10-342-844-78

Query Match      99.2%; Score 3829; DB 15; Length 871;
Best Local Similarity 100.0%; Pred. No. 3e-305;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSEGPAGGGEVAELPGDESGTPGGEAPFLSSLANLFEGEDGSLSPSPADASRPAGP 60
DB 1 MADSEGPAGGGEVAELPGDESGTPGGEAPFLSSLANLFEGEDGSLSPSPADASRPAGP 60
QY 61 GDGRNLRMKFQAGFRKGVNPNIDLLESTLYESSVVPKAPMDSLDYGYTRHSSDN 120
DB 61 GDGRNLRMKFQAGFRKGVNPNIDLLESTLYESSVVPKAPMDSLDYGYTRHSSDN 120
QY 121 KWRKKIIEKQPOSKPAPAPPPILKVFNRPILFDIVSRGSTADLDGLLPFLTHKKRL 180
DB 121 KWRKKIIEKQPOSKPAPAPPPILKVFNRPILFDIVSRGSTADLDGLLPFLTHKKRL 180
QY 181 TDEEPRESTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOT 240
DB 181 TDEEPRESTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOT 240
QY 241 ALHIAIERCKHYVELLVAQADVHAQARGREFQPKDEGGYFYFGEPLSLAACTNQPHI 300
DB 241 ALHIAIERCKHYVELLVAQADVHAQARGREFQPKDEGGYFYFGEPLSLAACTNQPHI 300
QY 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
DB 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
QY 361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDTRHLSRKPKDWAYGPVYSSLYD 420
DB 361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDTRHLSRKPKDWAYGPVYSSLYD 420
QY 421 LSSLDTCCEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYL 480
DB 421 LSSLDTCCEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYL 480
QY 481 AMVIFTLTAYQPLEGTPPYVRTTVDYLRAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
DB 481 AMVIFTLTAYQPLEGTPPYVRTTVDYLRAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
QY 541 NSLFDGSGFQLLYFYIYSLVIVSAALYLAGIEAYLAVVMVVALVGLWMNALYFTRGKLTG 600
DB 541 NSLFDGSGFQLLYFYIYSLVIVSAALYLAGIEAYLAVVMVVALVGLWMNALYFTRGKLTG 600
QY 601 TVSIMIQILFKDLPRFLLVYLLFMIGYASALVSLNPPCANMKVCNEDOTNCTVTPYPS 660
DB 601 TVSIMIQILFKDLPRFLLVYLLFMIGYASALVSLNPPCANMKVCNEDOTNCTVTPYPS 660
QY 661 RDSFTSFLLDLFKLTIGMGDLEMSLSTKYPVVFIIILVTVIILFTVLLNMLIALMGE 720
DB 661 RDSFTSFLLDLFKLTIGMGDLEMSLSTKYPVVFIIILVTVIILFTVLLNMLIALMGE 720
QY 721 TVGQVSKSKHIIWKLO 736
DB 721 TVGQVSKSKHIIWKLO 736
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RESULT 11
US-10-415-570A-2
; Sequence 2, Application US/10415570A
; Publication No. US20040198649A1
; GENERAL INFORMATION:
; APPLICANT: Davis, John Beresford
; APPLICANT: Gunthorpe, Martin James
; APPLICANT: Egerton, Julie
; APPLICANT: Smart, Darren
; TITLE OF INVENTION: New Use
; FILE REFERENCE: P32689
; CURRENT APPLICATION NUMBER: US/10/415,570A
; CURRENT FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: PCT/GB01/04739
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: GB 0026114.9
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-415-570A-2

Query Match      99.2%; Score 3829; DB 16; Length 871;
Best Local Similarity 100.0%; Pred. No. 3e-305;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSEGPAGGGEVAELPGDESGTPGGEAPFLSSLANLFEGEDGSLSPSPADASRPAGP 60
DB 1 MADSEGPAGGGEVAELPGDESGTPGGEAPFLSSLANLFEGEDGSLSPSPADASRPAGP 60
QY 61 GDGRNLRMKFQAGFRKGVNPNIDLLESTLYESSVVPKAPMDSLDYGYTRHSSDN 120
DB 61 GDGRNLRMKFQAGFRKGVNPNIDLLESTLYESSVVPKAPMDSLDYGYTRHSSDN 120
QY 121 KWRKKIIEKQPOSKPAPAPPPILKVFNRPILFDIVSRGSTADLDGLLPFLTHKKRL 180
DB 121 KWRKKIIEKQPOSKPAPAPPPILKVFNRPILFDIVSRGSTADLDGLLPFLTHKKRL 180
QY 181 TDEEPRESTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOT 240
DB 181 TDEEPRESTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOT 240
QY 241 ALHIAIERCKHYVELLVAQADVHAQARGREFQPKDEGGYFYFGEPLSLAACTNQPHI 300
DB 241 ALHIAIERCKHYVELLVAQADVHAQARGREFQPKDEGGYFYFGEPLSLAACTNQPHI 300
QY 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
DB 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
QY 361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDTRHLSRKPKDWAYGPVYSSLYD 420
DB 361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDTRHLSRKPKDWAYGPVYSSLYD 420
QY 421 LSSLDTCCEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYL 480
DB 421 LSSLDTCCEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYL 480
QY 481 AMVIFTLTAYQPLEGTPPYVRTTVDYLRAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
DB 481 AMVIFTLTAYQPLEGTPPYVRTTVDYLRAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
QY 541 NSLFDGSGFQLLYFYIYSLVIVSAALYLAGIEAYLAVVMVVALVGLWMNALYFTRGKLTG 600
DB 541 NSLFDGSGFQLLYFYIYSLVIVSAALYLAGIEAYLAVVMVVALVGLWMNALYFTRGKLTG 600
QY 601 TVSIMIQILFKDLPRFLLVYLLFMIGYASALVSLNPPCANMKVCNEDOTNCTVTPYPS 660
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Db      601 TYSIMQKILFKDLFRLLVLLFMIGVASALVSLNPCANNKVCNEDQTNCTVPTPSC 660
Qy      661 RDSFTSFLLDLFKLITGMGDMLSSTKYPVVFIIILLVTVIILTFVLLNMLIALMGE 720
Db      661 RDSFTSFLLDLFKLITGMGDMLSSTKYPVVFIIILLVTVIILTFVLLNMLIALMGE 720
Qy      721 TVGVSKESKHIWKLQ 736
Db      721 TVGVSKESKHIWKLQ 736

RESULT 12
US-10-027-828-2
; Sequence 2, Application US/10027828
; Publication No. US20030013650A1
; GENERAL INFORMATION:
; APPLICANT: Liedtke, Wolfgang
; APPLICANT: Heller, Stefan
; APPLICANT: Hudepeth, Albert J.
; APPLICANT: Friedman, Jeffrey M.
; TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC ACIDS E
; TITLE OF INVENTION: IT, AND USES THEREOF
; FILE REFERENCE: 600-1-287N
; CURRENT APPLICATION NUMBER: US/10/027,828
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/243,568
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-828-2

Query Match          99.2%; Score 3828; DB 14; Length 871;
Best Local Similarity 99.9%; Pred. No. 3.7e-305;
Matches 735; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MADSEGPAGGGEVAELPGDESGTGGGEAPFLSSLANLFEDEGSLSPSPADASRRPAG 60
Db      1 MADSEGPAGGGEVAELPGDESGTGGGEAPFLSSLANLFEDEGSLSPSPADASRRPAG 60
Qy      61 GDGRPNLRMKFQGAFRKGVNPNIDLESTLYESSVVPKAPMDSLPDYCTYRHHSSDN 120
Db      61 GDGRPNLRMKFQGAFRKGVNPNIDLESTLYESSVVPKAPMDSLPDYCTYRHHSSDN 120
Qy      121 KRWRKKIIEKQPSQPKAPAPQPPILKVFNRPILFDIVSRGSTADLDGLLPFLTHKKRL 180
Db      121 KRWRKKIIEKQPSQPKAPAPQPPILKVFNRPILFDIVSRGSTADLDGLLPFLTHKKRL 180
Qy      181 TDEEFREPSGTCTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSPPRDIYRGQT 240
Db      181 TDEEFREPSGTCTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSPPRDIYRGQT 240
Qy      241 ALHIAIERCKHYVELLVAQADVHAQARGFFQPKDEGGYFYFGEPLSLAACTNQPHI 300
Db      241 ALHIAIERCKHYVELLVAQADVHAQARGFFQPKDEGGYFYFGEPLSLAACTNQPHI 300
Qy      301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKCARLPFDS 360
Db      301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKCARLPFDS 360
Qy      361 NLEAVLNDGSLPLMAAKTKIGIFQHIIRREVTDETRHLSRKFKDWAYGPVYSSLYD 420
Db      361 NLEAVLNDGSLPLMAAKTKIGIFQHIIRREVTDETRHLSRKFKDWAYGPVYSSLYD 420
Qy      421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWKFKGAVSPYINWVSLC 480
Db      421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWKFKGAVSPYINWVSLC 480
Qy      481 AMVIFTLTAYOPLGTPPYRTTVDYLRAGEVITLFTGLVFFFTNIKDLFMKKCPGV 540

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Db      481 AMVIFTLTAYOPLGTPPYRTTVDYLRAGEVITLFTGLVFFFTNIKDLFMKKCPGV 540
Qy      541 NSLFDIDGSFQLLYIYISVLVIVSAALYLAGTEAVLAVMVFAVLGWMNALYFTRGLKLTG 600
Db      541 NSLFDIDGSFQLLYIYISVLVIVSAALYLAGTEAVLAVMVFAVLGWMNALYFTRGLKLTG 600
Qy      601 TYSIMQKILFKDLFRLLVLLFMIGVASALVSLNPCANNKVCNEDQTNCTVPTPSC 660
Db      601 TYSIMQKILFKDLFRLLVLLFMIGVASALVSLNPCANNKVCNEDQTNCTVPTPSC 660
Qy      661 RDSFTSFLLDLFKLITGMGDMLSSTKYPVVFIIILLVTVIILTFVLLNMLIALMGE 720
Db      661 RDSFTSFLLDLFKLITGMGDMLSSTKYPVVFIIILLVTVIILTFVLLNMLIALMGE 720
Qy      721 TVGVSKESKHIWKLQ 736
Db      721 TVGVSKESKHIWKLQ 736

RESULT 13
US-10-342-844-60
; Sequence 60, Application US/10342844
; Publication No. US20040009537A1
; GENERAL INFORMATION:
; APPLICANT: Roos, Jack
; APPLICANT: Stauderman, Kenneth
; APPLICANT: Velicelebi, G'n I
; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
; TITLE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCIUM
; FILE REFERENCE: 37481-3307
; CURRENT APPLICATION NUMBER: US/10/342,844
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/347,459
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/401,171
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/405,678
; PRIOR FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AAG28029
; DATABASE ENTRY DATE: 2000-10-31
US-10-342-844-60

Query Match          99.2%; Score 3828; DB 15; Length 871;
Best Local Similarity 99.9%; Pred. No. 3.7e-305;
Matches 735; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MADSEGPAGGGEVAELPGDESGTGGGEAPFLSSLANLFEDEGSLSPSPADASRRPAG 60
Db      1 MADSEGPAGGGEVAELPGDESGTGGGEAPFLSSLANLFEDEGSLSPSPADASRRPAG 60
Qy      61 GDGRPNLRMKFQGAFRKGVNPNIDLESTLYESSVVPKAPMDSLPDYCTYRHHSSDN 120
Db      61 GDGRPNLRMKFQGAFRKGVNPNIDLESTLYESSVVPKAPMDSLPDYCTYRHHSSDN 120
Qy      121 KRWRKKIIEKQPSQPKAPAPQPPILKVFNRPILFDIVSRGSTADLDGLLPFLTHKKRL 180
Db      121 KRWRKKIIEKQPSQPKAPAPQPPILKVFNRPILFDIVSRGSTADLDGLLPFLTHKKRL 180
Qy      181 TDEEFREPSGTCTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSPPRDIYRGQT 240
Db      181 TDEEFREPSGTCTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSPPRDIYRGQT 240
Qy      241 ALHIAIERCKHYVELLVAQADVHAQARGFFQPKDEGGYFYFGEPLSLAACTNQPHI 300
Db      241 ALHIAIERCKHYVELLVAQADVHAQARGFFQPKDEGGYFYFGEPLSLAACTNQPHI 300

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QY 301 VNYLTENPHKADMRDROSRGNTVHALVAADNTRENTKFTVMYDLLLLKCARLFPDS 360
 DB 301 VNYLTENPHKADMRDROSRGNTVHALVAADNTRENTKFTVMYDLLLLKCARLFPDS 360
 QY 361 NLEAVLNNDGLSPLMMAAKTKIGIFQHIIRREVTDTRHLSRKFKDWAYGVPVSSLYD 420
 DB 361 NLEAVLNNDGLSPLMMAAKTKIGIFQHIIRREVTDTRHLSRKFKDWAYGVPVSSLYD 420
 QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDWKRFKGFVAVSVINVSYLE 480
 DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDWKRFKGFVAVSVINVSYLE 480
 QY 481 AMVIFTLTAYTQPLEGTPPYRTTVDYLRAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
 DB 481 AMVIFTLTAYTQPLEGTPPYRTTVDYLRAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
 QY 541 NSLFDGFSQLLYFYISVIVSAALYLAGIEAYLAVMVFAVLGMMNALLYFTRGLKLTG 600
 DB 541 NSLFDGFSQLLYFYISVIVSAALYLAGIEAYLAVMVFAVLGMMNALLYFTRGLKLTG 600
 QY 601 TYSIMIQKILFKDLFRFLVLLFMIGYASALVSLNPNCAKMKVCNEDQTNCTVPTPSC 660
 DB 601 TYSIMIQKILFKDLFRFLVLLFMIGYASALVSLNPNCAKMKVCNEDQTNCTVPTPSC 660
 QY 661 RDSETFSTFLDLFKLTIGMGDLEMLSTKYPVVFIIILLVTVIILLTFVLLNMLIALMGE 720
 DB 661 RDSETFSTFLDLFKLTIGMGDLEMLSTKYPVVFIIILLVTVIILLTFVLLNMLIALMGE 720
 QY 721 TVGQVSKESKHIWKIQ 736
 DB 721 TVGQVSKESKHIWKIQ 736

RESULT 14
 US-10-027-828-4
 ; Sequence 4, Application US/10027828
 ; Publication No. US20030013650A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liedtke, Wolfgang
 ; APPLICANT: Heller, Stefan
 ; APPLICANT: Hudspeeth, Albert J.
 ; APPLICANT: Friedman, Jeffrey M.
 ; TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC ACIDS H
 ; FILE REFERENCE: 600-1-287N
 ; CURRENT APPLICATION NUMBER: US/10/027,828
 ; PRIOR FILING DATE: 2001-10-25
 ; PRIOR FILING DATE: 2000-10-26
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 871
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-027-828-4

Query Match 99.1%; Score 3825; DB 14; Length 871;
 Best Local Similarity 99.9%; Pred. No. 6.4e-305;
 Matches 735; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MADSEGPAGGGEVAELPGDESGTPGGEAPPLSSLANLFEDEGSLSPSPADASRRPAGP 60
 DB 1 MADSEGPAGGGEVAELPGDESGTPGGEAPPLSSLANLFEDEGSLSPSPADASRRPAGP 60
 QY 61 GDGRNLRMKFOGAFKRGVNPIDILESTLYESSVVPKAPMDSLFDYGYRHHSSDN 120
 DB 61 GDGRNLRMKFOGAFKRGVNPIDILESTLYESSVVPKAPMDSLFDYGYRHHSSDN 120
 QY 121 KWRKXIIIEKQPSKAPAPPPILKVFNRPIFDIVSRGSTADLGLLPFLTHKKRL 180
 DB 121 KWRKXIIIEKQPSKAPAPPPILKVFNRPIFDIVSRGSTADLGLLPFLTHKKRL 180

QY 181 TDEFRPESTGKTCIPLKALLNLSGRNDTIPVLLDIAERTGNMREFINSPPRDIYRGOT 240
 DB 181 TDEFRPESTGKTCIPLKALLNLSGRNDTIPVLLDIAERTGNMREFINSPPRDIYRGOT 240
 QY 241 ALHIAIRERRCHYVELLVAQADVHAQARGFPQKDEGGYFYFGELPLSLAACTNQPHI 300
 DB 241 ALHIAIRERRCHYVELLVAQADVHAQARGFPQKDEGGYFYFGELPLSLAACTNQPHI 300
 QY 301 VNYLTENPHKADMRDROSRGNTVHALVAADNTRENTKFTVMYDLLLLKCARLFPDS 360
 DB 301 VNYLTENPHKADMRDROSRGNTVHALVAADNTRENTKFTVMYDLLLLKCARLFPDS 360
 QY 361 NLEAVLNNDGLSPLMMAAKTKIGIFQHIIRREVTDTRHLSRKFKDWAYGVPVSSLYD 420
 DB 361 NLEAVLNNDGLSPLMMAAKTKIGIFQHIIRREVTDTRHLSRKFKDWAYGVPVSSLYD 420
 QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDWKRFKGFVAVSVINVSYLE 480
 DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDWKRFKGFVAVSVINVSYLE 480
 QY 481 AMVIFTLTAYTQPLEGTPPYRTTVDYLRAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
 DB 481 AMVIFTLTAYTQPLEGTPPYRTTVDYLRAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
 QY 541 NSLFDGFSQLLYFYISVIVSAALYLAGIEAYLAVMVFAVLGMMNALLYFTRGLKLTG 600
 DB 541 NSLFDGFSQLLYFYISVIVSAALYLAGIEAYLAVMVFAVLGMMNALLYFTRGLKLTG 600
 QY 601 TYSIMIQKILFKDLFRFLVLLFMIGYASALVSLNPNCAKMKVCNEDQTNCTVPTPSC 660
 DB 601 TYSIMIQKILFKDLFRFLVLLFMIGYASALVSLNPNCAKMKVCNEDQTNCTVPTPSC 660
 QY 661 RDSETFSTFLDLFKLTIGMGDLEMLSTKYPVVFIIILLVTVIILLTFVLLNMLIALMGE 720
 DB 661 RDSETFSTFLDLFKLTIGMGDLEMLSTKYPVVFIIILLVTVIILLTFVLLNMLIALMGE 720
 QY 721 TVGQVSKESKHIWKIQ 736
 DB 721 TVGQVSKESKHIWKIQ 736

RESULT 15
 US-10-090-215-7
 ; Sequence 7, Application US/10090215
 ; Publication No. US20030032097A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dubin, Adrienne E
 ; APPLICANT: Huvar, Arne
 ; APPLICANT: Erlander, Mark G
 ; APPLICANT: Glass, Charles A
 ; TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor
 ; TITLE OF INVENTION: VR3
 ; FILE REFERENCE: Human VR3 receptors
 ; CURRENT APPLICATION NUMBER: US/10/090,215
 ; CURRENT FILING DATE: 2002-03-04
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 871
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-090-215-7

Query Match 99.1%; Score 3823; DB 14; Length 871;
 Best Local Similarity 99.9%; Pred. No. 9.4e-305;
 Matches 735; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MADSEGPAGGGEVAELPGDESGTPGGEAPPLSSLANLFEDEGSLSPSPADASRRPAGP 60
 DB 1 MADSEGPAGGGEVAELPGDESGTPGGEAPPLSSLANLFEDEGSLSPSPADASRRPAGP 60
 QY 61 GDGRNLRMKFOGAFKRGVNPIDILESTLYESSVVPKAPMDSLFDYGYRHHSSDN 120

Db 61 GDGRNLRMKFGAPRKGVNPNIDLLESTLYESSVVGPKKAPMDSLFYGYTRHSSDN 120
Qy 121 KWRKXIIEKQSPKAPOPPPILKYFNRPILFDIVSRGSTADLDGLIPFLTHKKRL 180
Db 121 KWRKXIIEKQSPKAPOPPPILKYFNRPILFDIVSRGSTADLDGLIPFLTHKKRL 180
Qy 181 TDEEPREPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOT 240
Db 181 TDEEPREPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOT 240
Qy 241 ALHIAIERCKHYVELLVAQGAHVHAQARGFFQPKDEGGYFYFGEPLSLAACTNQPHI 300
Db 241 ALHIAIERCKHYVELLVAQGAHVHAQARGFFQPKDEGGYFYFGEPLSLAACTNQPHI 300
Qy 301 VNYLTENPHKADMRQDSRGNTVLHALVADNTRENTKFTVMYDILLKCARLPDS 360
Db 301 VNYLTENPHKADMRQDSRGNTVLHALVADNTRENTKFTVMYDILLKCARLPDS 360
Qy 361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDTRHLSRKFKDWAYGPVYSSLYD 420
Db 361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDTRHLSRKFKDWAYGPVYSSLYD 420
Qy 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLE 480
Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLE 480
Qy 481 AMVIFTLTAYYQPLEGTPPYRTTVDYLRAGEVITLFTGVLPFFTNIKDLFMKCKCGV 540
Db 481 AMVIFTLTAYYQPLEGTPPYRTTVDYLRAGEVITLFTGVLPFFTNIKDLFMKCKCGV 540
Qy 541 NSLFDGSGFQLLYFTYSVLVIVSAALYLAGIEAYLVAVVFAVLVGMNALLYFTRGLKLTG 600
Db 541 NSLFDGSGFQLLYFTYSVLVIVSAALYLAGIEAYLVAVVFAVLVGMNALLYFTRGLKLTG 600
Qy 601 TYSIMIQILFKDLFRFLVYLLFMIGYASALVSLNPNCANMKVCNEDQTNCTVPTYPSC 660
Db 601 TYSIMIQILFKDLFRFLVYLLFMIGYASALVSLNPNCANMKVCNEDQTNCTVPTYPSC 660
Qy 661 RDSETFSTFLDLFKLTIGMGDLEMLSTKYPVVFIIILLVYIILTFVLLANMLIALMGE 720
Db 661 RDSETFSTFLDLFKLTIGMGDLEMLSTKYPVVFIIILLVYIILTFVLLANMLIALMGE 720
Qy 721 TVGVSKESKHIWKIQ 736
Db 721 TVGVSKESKHIWKIQ 736

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OM protein - protein search, using sw model

Run on: May 4, 2005, 22:08:03 ; Search time 21 Seconds
(without alignments)
3399.659 Million cell updates/sec

Title: US-10-090-215-12

Perfect score: 3858

Sequence: 1 MADSEGPRAQGEVAELPG.....QVSKESKHIWKLQSGRRRL 742

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1579.5	40.9	838	T09054	capsaicin receptor
2	1551.5	40.2	839	JC7621	capsaicin receptor
3	736.5	19.1	727	JC7796	epithelial calcium
4	724.5	18.8	725	JC7531	calcium transport
5	719	18.6	723	JC7795	epithelial calcium
6	473.5	12.3	937	T37241	olfactory channel
7	473.5	12.3	957	D88651	protein B0212.5 (i
8	435.5	11.3	900	T33026	hypothetical prote
9	313.5	8.1	790	T20312	hypothetical prote
10	278	7.2	519	T24772	hypothetical prote
11	204.5	5.3	1188	T19552	hypothetical prote
12	188	4.9	828	JC5807	trp3 protein - rat
13	145.5	3.8	1124	JH0588	calmodulin-binding
14	138.5	3.6	810	T18361	TRPC1 protein - hu
15	137	3.6	616	T00894	hypothetical prote
16	137	3.6	1765	T42388	sodium channel alp
17	136.5	3.5	683	A85044	hypothetical prote
18	136	3.5	2352	T30201	Notch homolog prot
19	134	3.5	1275	JU0092	trp protein - frui
20	133	3.4	481	T23729	hypothetical prote
21	132	3.4	1274	JN0015	trp protein - frui
22	131.5	3.4	642	S58154	hypothetical prote
23	130.5	3.4	652	D85044	hypothetical prote
24	129.5	3.4	608	G02640	polycystic kidney
25	129	3.3	823	S44873	ZC21.2 protein - C
26	127.5	3.3	4377	A55575	ankyrin 3, long sp
27	126.5	3.3	643	D86167	protein F21B7.27
28	126.5	3.3	2471	A49128	cell-fate determin
29	126	3.3	2212	A41098	calcium channel pr

30	125.5	3.3	934	1	H71274	probable ankyrin -
31	125.5	3.3	2529	2	B64635	toxin-like outer m
32	125	3.2	1957	2	S68453	sodium channel pro
33	124	3.2	793	2	S68238	trp-1 protein - hu
34	123.5	3.2	968	2	A37867	transcription fact
35	123	3.2	751	2	F85043	hypothetical prote
36	123	3.2	2531	2	T31070	notch homolog - se
37	121	3.1	488	2	JC7995	transient receptor
38	121	3.1	1549	2	T13940	ankyrin - fruit fl
39	120.5	3.1	397	2	T46445	hypothetical prote
40	120.5	3.1	573	2	D86464	FL2G12.13 protein
41	120.5	3.1	664	2	A56695	notch2 protein hom
42	120	3.1	633	2	T27499	hypothetical prote
43	119.5	3.1	574	2	T47566	hypothetical prote
44	119	3.1	1765	2	T42714	ankyrin 3, splice
45	119	3.1	1940	2	T42715	ankyrin 3, splice

ALIGNMENTS

RESULT 1

T09054

capsaicin receptor - rat

N:Alternate names: vanilloid receptor subtype 1

C:Species: Rattus norvegicus (Norway rat)

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C:Accession: T09054

R:Caterina, M.D.; Schumacher, M.A.; Tominaga, M.; Rosen, T.A.; Levine, J.D.; Julius, D.

Nature 389, 816-824, 1997

A:Title: The capsaicin receptor: A heat-activated ion channel in the pain pathway.

A:Reference number: Z16539; MUID:98007969; PMID:9349813

A:Accession: T09054

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-838 <CAT>

A:Cross-references: UNIPROT:O35433; EMBL:AF029310; NID:g2570932; PIDN:AAC53398.1; PID:g2:

A:Experimental source: dorsal root ganglion

C:Keywords: ion channel; receptor

Query Match 40.9%; Score 1579.5; DB 2; Length 838;
Best Local Similarity 44.6%; Pred. No. 1.1e-103;
Matches 338; Conservative 129; Mismatches 193; Indels 97; Gaps 16;

QY	16	AELPGDESGTQGE-----	APLSSLANLFEGRDGLSPSPADA 54
DB	5	ASLDESESPQENSCLDPPDRDNCPPVKPHIFTRSTRLF-GKGDSEASPLDC 63	
QY	55	SRPAGPGDGRPNLRMKQGAFAKGVN-PIDLLESTLYESSVVGPKKAPMDSLFYGYT 113	
DB	64	PVEEG-----GLASCPITVSSVL---TIQRPDGGP-----ASV 94	
QY	114	RHSSDNKRWRKRIIEKQSPKAPAPQPPILKVPNRPILFDIVSRGSTADLDGLLPL 173	
DB	95	RPSSQDS-----VSAGEKPP--RLYDRRSIFDAVAQSCQLESLLPL 136	
QY	174	LTHKKRLTDEPREPGTKCLPKALLNLNGRNTIPVLLDIAERTGNMRFFINSPPRD 233	
DB	137	QRSKRLTDSPEKDPETGKTCLLKALNLHNGQNTIALLLDVARKTSLKGFVNASYTD 196	
QY	234	IYRQQTALHIAIERRRCKHYVELLVQAQADVHAQGRFFQPKDEGGYFYFGELPLSLAA 293	
DB	197	SYKQQTALHIAIERNNMTLVLLVENGADVQAAANGDFKTKGRPGFYFGELPLSLAA 256	
QY	294	CYNQPHIVNYLTENPHKAMRRQSRGNTVULHALVAIDNTRENTKFTKMYDLKLLKC 353	
DB	257	CTNQLAIKFKLLQNSWQPADISARDSVGNVLHALVEADNTVDNTKFTVSMYNEILLG 316	
QY	354	RELFPDSNLEAVLNNDGLSPLMMAKTGKIGIFQHIIRREVTDETRHLSRKFQWAGP 413	
DB	317	AKLHPTLKLEETNRKGLTPLAALASSGKIGVLAVILOREIHEPECRHLSRKFTEWAYGP 376	
QY	414	VYSSLYDLSSLDTCGEASVLEILVY-NSKIENRHEMLAVEPINELLRDKRKFQVSVFY 472	


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Db 120 ALHIAVINQNVNLRALLARGASVSARATGVSFHYRPH-NLIYYGEHPLSPAACVGSBEI 178
Qy 301 VNYLTENPHKKADMRQDSRGNTVHALVAADNTRENTKFTVMYDILL-----LKC 353
Db 179 VRLIEH---GADIRAQDSLGNTVLHLI-----LQPNKTFACQMYNLLSYDGGDLK- 229
Qy 354 ARLPDPSNLEAVLNNDGSLPMAAKTGKIGIFOHIIIRREVTDTRHLSRKFDMWAYGP 413
Db 230 -----SLELVPNNOGLTPFKLAGVEGNIVMFQHLMOK-----RKHIQWTYGP 271
Qy 414 VYSSLYDSSLDTCGERASVLEILVYNKSKIEHRLAVALPEINELLRRDKWRKFGASVFI 473
Db 272 LTSTLYDLTEIDSGDQDSLELITVTKKREAR-QILDQTPVKELSVLKXRYGRPYFCV 330
Qy 474 NVVSVLCAMVIFTTAYYOPE-----GTPP-----PYRTTVLYRLAGEVI 516
Db 331 LGALVLYIICFTWCVCVRPLKPRITNTRPNRNTLMQOKLQEAAYTPKDDLRLVGLV 390
Qy 517 LFTGVLFNFTNIKDLFMKKCPGVNSLF-----IDGSFOLLFYIYVSVLVSAALYLAGIE 572
Db 391 SIUGAVIILLVEIPDLPL---GVTRFFGQTILGGPFPHVITVAFVVLVTVMRLTNVD 447
Qy 573 AYLAVMFALVGMNVALYFTRGLKLTGTYSIMIOKILFKDLFPELLVYLFMIGYASAL 632
Db 448 GEVVPMSFALVGMNVMYFARGFQMLGPFITIMIQMIFGDLRFCLMMAVVILGFASAF 507
Qy 633 VSLNPNCANMKVCNEDQNC-TVTPYPSCRDSETFSTFLDLFLKLTIGMG---DLEMLS 687
Db 508 YIIFO-----TEDPDELGHFYDYPMA-----LFSTF---ELF-LTIIDGPANYDVDL-- 550
Qy 688 STKPVVFIILLVYIITLVFLLNMLIALMGETVGVSKESKHIWKLQ 736
Db 551 ----PFMYSVTYAAFAIATLMLNLLIAMMGDTHWRVAHERDELWRAQ 595

RESULT 4
JC7531
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7531
R;Peng, J.B.; Chen, X.; Berger, U.V.; Weremowicz, S.; Morton, C.C.; Vassilev, P.M.; Brown
Biochem. Biophys. Res. Commun. 278, 326-332, 2000
A;Title: Human calcium transport protein Cat1.
A;Reference number: JC7531; MUID:20551480; PMID:11097838
A;Accession: JC7531.
A;Molecule type: mRNA
A;Residues: 1-725 <PEN>
A;Cross-references: UNIPROT:Q9H296; GB:AF304463
C;Comment: This protein, a member of a family of Ca2+ channels, has a role in cellular c
ine and kidney.
C;Genetics:
A;Gene: Cat1
A;Map position: 7q33-34
C;Keywords: calcium channel; calcium transport; intestine; kidney; transmembrane protein

Query Match 18.8%; Score 724.5; DB 2; Length 725;
Best Local Similarity 32.9%; Pred. No. 3.1e-43;
Matches 198; Conservative 98; Mismatches 218; Indels 87; Gaps 20;

Qy 171 PFLTHK-----KRLTDEEFR---BPSTGKTCCLPKALL--NLSNGRNDTIPVLLDIA 217
Db 48 PULLAANDVQALNKLKYEDCKVHHRGANGETALHIAALYDNL-----EAAVLMSEA 102
Qy 218 ERTGNMREFINSPPFDIYYRGQTALHIAIERCKHYVELLVAQADVAQAGRFQPKD 277
Db 103 P-----ELVPEPMTSELYEGQTALHIAVQNMNVLRAALLARRASVSARATGTAFR-RS 155
Qy 278 EGGYPYFELPLSLAACNTQPHIVNYLTENPHKKADMRQDSRGNTVHALVAADNTRE 337
Db 156 PCNLIIYFGEHPLSPAACVNSEIIVRLIEH---GADIRAQDSLGNTVLHLI-----LQP 207
Qy 338 NTKFTVYMYDILLKLCARLFPDSNLEAVLNNDGSLPMAAATGKIGIFOHIIIRREVTD 397

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Db 208 NKTACQMYNLLSYDRHGHLOPLDLVPHNQGLTPFKLAGVEGNTVMFQHLMOK----- 262
Qy 398 DTRHLSRKFDMWAYGPVYSSLYDSSLDTCGERASVLEILVYNKSKIEHRLAVALPEIN 457
Db 263 -----RKHIQWTYGPSTLYDTEIDSGDQDSLELITVTKKREAR-QILDQTPVK 315
Qy 458 LLRDWRKFGASVFIYINNVSVLCAMVIFTTAYYOPE-----GTPP-----Y 500
Db 316 LVSLKWKRYGRPYFCMLGALVLYIICFTWCVCVRPLKPRITNTRPNRNTSPPDNTLLQKLQ 375
Qy 501 PYRTTVLYRLAGEVIITLFTGVLFNFTNIKDLFMKKCPGVNSLF-----IDGSFOLLFYIY 556
Db 376 AYMTPKDRIRLVGLSVTVIGAIILLLVEVPDIFR---GVTRFFGQTILGGPFPHVLIITY 432
Qy 557 SVLVIVSAALVLAGIEAVLVGMNVALYFTRGLKLTGTYSIMIOKILFKDLFR 616
Db 433 AFMLVLTVMRLNLSASGEVVPMSFALVGMNVMYFARGFQMLGPFITIMIQMIFGDLMR 492
Qy 617 FLLVYLLFMIGYASALVSLNPNCANMKVCNEDQNC-TVTPYPSCRDSETFSTFLDLFLK 675
Db 493 FCMLMAVVILGFASAFYIIFO-----TEDPDELGHFYDYPMA-----LFSTF---ELF- 537
Qy 676 LTIQMGDLEMLSSSTKYVPVFIILLVYIITLVFLLNMLIALMGETVGVSKESKHIWKL 735
Db 538 LTIIDGPANY--NVDLPFMSITYAAFAIATLMLNLLIAMMGDTHWRVAHERDELWRA 595

736 Q 736
596 Q 596

RESULT 5
JC7795
epithelial calcium channel 1, ECaC1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 02-Apr-2002
C;Accession: JC7795
R;Weber, K.; Erben, R.G.; Rump, A.; Adamski, J.
Biochem. Biophys. Res. Commun. 289, 1287-1294, 2001
A;Title: Gene structure and regulation of the murine epithelial calcium channels ECaC1 a
A;Reference number: JC7795
A;Accession: JC7795
A;Molecule type: DNA
A;Residues: 1-723 <WEB>
A;Cross-references: GB:AF336378
C;Comment: This calcium channel plays an important role in active transcellular calcium e
relevant for in vivo calcium homeostasis.
C;Genetics:
A;Gene: ECaC1
A;Map position: 6
A;Introns: 37/2; 70/1; 111/1; 157/1; 190/1; 247/3; 296/3; 367/3; 422/2; 477/3; 501
C;Keywords: calcium channel

Query Match 18.6%; Score 719; DB 2; Length 723;
Best Local Similarity 33.3%; Pred. No. 7.6e-43;
Matches 201; Conservative 100; Mismatches 198; Indels 104; Gaps 23;

Qy 173 LLTHKRLTDE--EPRE--PSTGKTCCLPKALL--NLSNGRNDTIPVLLD-----IAERTGN 222
Db 52 MCTLKQLQHQDCDFRQFGALGETALHVAALYDNL-----DAAIMLEAAPVLTTEST-- 104
Qy 223 MREFINSPPFDIYYRGQTALHIAIERCKHYVELLVAQADVAQAGRFQPKDGGYF 282
Db 105 ----LCEPF-----VGQTALHIAVQNMNVLRAALLARGASARATGSAPH-RSHNLI 154
Qy 283 YFGEHPLSLAACNTQPHIVNYLTENPHKKADMRQDSRGNTVHALVAADNTRENTKPV 342
Db 155 YFGEHPLSFAACVNSEIIVRLIEH---GADIRAQDSLGNTVLHLV-----LQPNKTPA 206
Qy 343 TKMYDILL-----LKCARLFPDSNLEAVLNNDGSLPMAAATGKIGIFOHIIIRREV 395
Db 207 CQMYNLLSYDGGDLK-----SLELVPNNOGLTPFKLAGVEGNTVMFQHLMOK----- 255

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Db 486 ----LLCIPFLMKHEIE--ALFVFALPGSWIFLFFARSAKLTGPFVQMIYSGIAD 539
 Qy 614 LFRPLVLLFMIGVASALVSU-LNPCANMKVCNEDQINC-----TVTPYSCRDSETF 667
 Db 540 MIRFAIIISAIFLVSQVFFYFGKMDAKQKLEDNPNACRISGVTIYV-----NTPP 593
 Qy 668 TFLDLFKLTIGMGDLEMLSTKYPVFIILVTVIILTFVLLNMLIALMGVETGVQVSK 727
 Db 594 EFTIFLFRASMGYDYEFSCANYQALTKTLFVLYMFVMPIMINILLIAMGNTVTVIA 653
 Qy 728 ESKHIWKLO 736
 Db 654 QAEKAWROQ 662

RESULT 8
 T33026
 hypothetical protein T09A12.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T33026
 R:Hawkins, J.; Fulton, B.; Gillam, B.
 submitted to the EMBL Data Library, February 1998
 A:Description: The sequence of C. elegans cosmid T09A12.
 A:Reference number: Z21265
 A:Accession: T33026
 A>Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-900 <HAW>
 A:Cross-references: UNIPROT:O61220; EMBL:AF047660; PIDN:AA04431.1; GSPDB:GN000022; CESP:
 A:Experimental source: strain Bristol N2; clone T09A12
 C:Genetics:
 A:Gene: CESP:T09A12.3
 A:Map position: 4
 A:Introns: 43/2; 86/3; 260/2; 396/3; 424/2; 495/1; 517/3; 553/3; 691/3; 741/3; 780/3; 82

Query Match 11.3%; Score 435.5; DB 2; Length 900;
 Best Local Similarity 24.9%; Pred. No. 1.2e-22;
 Matches 167; Conservative 99; Mismatches 231; Indels 173; Gaps 26;
 Qy 189 STGKTCPLKALNLNGRNDTIPVLLDIAERTGNMREFINSFRIY----YRGQTALHI 244
 Db 154 SMGTIIGCLLHSDIHNALVLKILDYVKKLN-----DIHISEDYGLSPLHQ 203
 Qy 245 A-IERRCKHYVELLAQADVHAQARGRFQPKDE-----GGYF 282
 Db 204 AIINTDCK-LVYKFLKLGADVNSRCYGAFFCADDQKASRTDSLEHYVELSLKNTYGNM 262
 Qy 283 YFGLPLSLAACTNQHIVNYLTENPHKADMRQDSRGNTVHLVAIAADNTRENTKRV 342
 Db 263 YLGEPLSFAACLNQPSFRLLA---PKANPAQDTNGNSVLMCV-----IHENMAMF 314
 Qy 343 TKMYDLLLLKCARLPDSNLEAVLNNDGLSPLMAAKTGKIGIFOHIIIRREVTDTRHL 402
 Db 315 K-----LALECG-----ASLRTV-NKQSLSPULLAAKLAKEMFDBILEGDSV----- 358
 Qy 403 SRKFDWAYGPVSSLYDLSSLDTCGE-----EASVLEILVYNSKIENRHEMLAVEPIN 456
 Db 359 -----WAYGDASSTAYPLAKIDTINETTGELNEASALSLVYGVQTE--HLELDGLLD 410
 Qy 457 ELLRDKWRKFG-----AVSFYINNVSVLCAMVIFTL-----TAYYQPLEG- 496
 Db 411 TLLEAKWEAFKRNWIVSFTATLYICVTAFTLRPGFSTEMLTGWINRYSFPFGR 470
 Qy 497 -----TPPYFRTVDYLRAGE---VI 516
 Db 471 YGKNSTLQQKQKVINATSRGLVWSEPLSQCHLRNWDPDIPFANS--YIRLVFELFVVI 528
 Qy 517 TLFTGVLPFFTNKDLFMKKCGVNSLP-IDGSFQLLYFIYSVLVVSAALYAGIBAVL 575
 Db 529 GICVQVFLDFRDIKRGKKNWNLTAFFPAKITFKLTVPLVLAIMPTRLACDLSPLVAV 588

Qy 576 --AVNVFALVIGMNALYFTRGLKLTGTYSIMQKILFKDLFRLLVLLFMIGVASALV 633
 Db 589 DNVLITVTMIETVHYLYCYRIVREVGPFVLMVYTIATDIPRFLMIYIGIFLMGFSQSF 648
 Qy 634 SLLNPG---AN-MKVCNEDQINCT-----VPTYSC--RDSSTES----- 667
 Db 649 LIFUSCREANVKKLITDQSEASGSKNKNLTKQISAYDTAIVKNAEVFENVNQSPIE 708
 Qy 668 ----TFLDLFKLTIGMGDLEMLSTKYPVFIILVTVIILTFVLLNMLIALMG---E 720
 Db 709 AFVRTILITIGFTVLYENLALCPANTVMWIKVVFILFELFVSIQFNMLIAMTTRTYE 768
 Qy 721 TVGQVSKESK 730
 Db 769 TIFQTQLEYK 778

RESULT 9
 T20312
 hypothetical protein F28H7.10 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T20312; T21533
 R:Mathews, P.
 submitted to the EMBL Data Library, June 1996
 A:Reference number: Z19255
 A:Accession: T20312
 A>Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-790 <WIL>
 A:Cross-references: UNIPROT:P90784; EMBL:Z74030; PIDN:CAA98449.1; GSPDB:GN000023; CESP:F2E
 A:Experimental source: clone D1054
 R:Berks, M.
 submitted to the EMBL Data Library, May 1996
 A:Reference number: Z19435
 A:Accession: T21533
 A>Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-790 <W12>
 A:Cross-references: EMBL:Z72508; PIDN:CAA96644.1; GSPDB:GN000023; CESP:F28H7.10
 A:Experimental source: clone F28H7
 C:Genetics:
 A:Gene: CESP:F28H7.10
 A:Map position: 5
 A:Introns: 46/2; 89/3; 129/1; 157/1; 201/1; 264/2; 349/3; 406/3; 487/3; 543/2; 580/1; 675

Query Match 8.1%; Score 313.5; DB 2; Length 790;
 Best Local Similarity 22.0%; Pred. No. 4.4e-14;
 Matches 155; Conservative 94; Mismatches 209; Indels 245; Gaps 28;
 Qy 152 PTFDIVSRGSTADLDGLLPFLTHKKEL-----TDEEPE-----PSTCK 192
 Db 109 ENILDEFQGO-AEWAGDL-----KKALKLDGGGKGKSKSEKREMWVSVDERGSMGE 161
 Qy 193 TCLPKALNLNGRNDTIPVLLDIAERTGN-MREFINSFRIYVYRGQTAHIAIERRCK 251
 Db 162 NLLATCLLQGSALHN-----LIARRLINPPKLINDICVSEYVGLSPLHLAIWNQDA 214
 Qy 252 HYVELLVAQADVHAQARGRFQPKDE-----GGYFYGELPLS 290
 Db 215 QFTSLRLGLADLNQRCYGAFFCADDQKASRTDSLEHBEFVELTKNTNTYTGSMYFGEYPLS 274
 Qy 291 LAACCTNQHIVNYLTENPHKADMRQDSRGNTVHLVAIAADNTRENTKFTVYQVYDLLL 350
 Db 275 FAICMGQHDLFRLMLA---KXANLSAQDTNGNTALH-LCVIHD-----KM-DMU- 318
 Qy 351 LKCARLPDSNLEA-----VLNNDGLSPLMAAKTGKIGIFOHIIIRREVTDTRHLSK 405
 Db 319 -----DAVLEAGNIRLANKQNLTAALAK-----KTESIQHLE-- 356
 Qy 406 FKDWAYGPVSSLYDLSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRK 465
 Db 357 -----LMDGLIEQLDEKWA 372

QY 466 FGAVSFYINVSYLCAWIFLTITAYYQLEGTPPYRTTVD----- 507
Db 373 YGRALWRLSLGFIFFYCCFVCAWMLRSPSSATTEHLTRINDGEGESTNSTNYLOWHA 432
QY 508 -----YLRAGEVILFT---GVLFFFTNIKDL-----FMKKCPG 539
Db 433 IDTOCHLMYYSAPWGHGFRGLGCEIMIIIVMLFOILLDFGDIRIGFKQWFLKAFPA 492
QY 540 VNSLFIDGSPQLLYPIYVSVLSAALYAGIEAVLAV---MVPALVIGWNNALYFTRG 595
Db 493 ---KLMFKGAF--LFTIISIPCLACSPH---EPELTDNTMAIISILLVTHQHFLLYMYRA 544
QY 596 LKLTCTYSIMQIKFLDFLLFLVLLFMIGYASALVSLNPNCAVMKVCNEDQINCIVP 655
Db 545 IPFVGPFVLMVTIATDLVRFAMIYSFLVGFSSFLYFTSCB----- 589
QY 656 TYPSCRDSETF-----STF-----LLDLFKLTIGMDL---EMLSSTKYPVVF 695
Db 590 -----RDSTAICKIDPMGSEFNMINENPVDALLRTFIMTIGFVSFLYREMSACDNFWMKW 644
QY 696 ILLVTVIILFVLL--NMLIALMG---ETVGQVSKSKHIW 733
Db 645 IGKLFVFIFETVSILOFNLLIAMTRTYETIFLTRKEWKQW 687

RESULT 10
T24772
hypothetical protein T10B10.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24772
R:Sing, M.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z19934
A:Accession: T24772
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-519 <WIL>
A:Cross-references: UNIPROT:Q22374; EMBL:Z72514; PIDN:CAA96679.1; GSPDB:GN000028; CESP:T10B10.7
A:Experimental source: clone T10B10
C:Genetics:
A:Map position: X
A:Introns: 47/3; 139/1; 183/1; 215/2; 249/2; 385/3; 440/3

Query Match 7.2%; Score 278; DB 2; Length 519;
Best Local Similarity 29.5%; Pred. No. 7.9e-12;
Matches 89; Conservative 36; Mismatches 115; Indels 62; Gaps 10;

QY 216 IAEITGNREFINSFP-RDIYR--GQALHAIERRCKHYVELLVAGADVHAQARGRF 272
Db 161 VKQMYRPFKIVNIFLSEETIASVGLSPLHQAVNEDLEWVYLCRGADVHORCYGSF 220
QY 273 FQPKDE-----GGYFYFGELPLSLAACTNQPHIVNLTENPHKK 311
Db 221 FCADDQKASRTDLSLEHWVDLVQSTKYTGQYWGSEYPLSFAACTNQVDFLLRA--MK 277
QY 312 ADMRRQDRGNTVLHVAIAIDNTRENTKFTVKMYDLLLLCARLPDPSNLEAVLNNDGL 371
Db 278 ADPNMPDNTNGNTVLH-----LTVIHDLPMEFMLEAVELGANLH-VRNNLKL 321
QY 372 SPLMAAKTGKIGIFQHIIRREVTDTRHLSRKFQKWAYGVPYSSLYDLSLDTCCGE- 430
Db 322 TPLAALAAKHHYDLLE---CMDI-----SWRYGPVCKAYPLNDVDTINESD 370
QY 431 -----ASVLEILVNSKINRHEMLAVBPINELLRDKWRKFGAVSFYINVSYLCAWIF 485
Db 371 GSLNPNSVIANVYGDKVD--HLEPFDGLIEVLESKWETGKKOLFMSLAGIYFLAVF 428
QY 486 TL 487
Db 429 YL 430

RESULT 11

T19552
hypothetical protein C29B6.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T19552
R:Johnson, R.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z19141
A:Accession: T19552
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1188 <WIL>
A:Cross-references: UNIPROT:Q18297; EMBL:Z72504; PIDN:CAA96603.1; GSPDB:GN000022; CESP:C29B6
A:Experimental source: clone C29B6
C:Genetics:
A:Gene: CESP:C29B6.2
A:Map position: 4
A:Introns: 147/2; 473/3; 500/1; 529/1; 584/2; 688/2; 839/3; 975/3; 1132/3

Query Match 5.3%; Score 204.5; DB 2; Length 1188;
Best Local Similarity 20.3%; Pred. No. 4.1e-06;
Matches 152; Conservative 98; Mismatches 250; Indels 247; Gaps 33;

QY 124 RKKLIEKQPSKAPAPQPPPIKVFNRPIILFDIVSRGSTADLD-----GLLPFLLT 175
Db 418 RKNKETERSALKSPTRNTLRIVSEDRVRTVMNVDRDQNTPMHIVASNGYLEMMQLLOK 477
QY 176 HKKRLT---DEEPREPSTGKCLPKALLNL-----TALHRAIGVROLLEWDIRLLMKDEGNSALHLAARSG 529
Db 478 HGASITQVNEDEE-----TALHRAIGVROLLEWDIRLLMKDEGNSALHLAARSG 529
QY 206 RNDTIPVLLDIAERTGNMREFINSFPRDIYRGOTALHAIERRCKHYVELLVAGADVH 265
Db 530 HDATTKVLLD---NGADKEAKNS-----YQ-KTPLQVAVDSGKLETCQRLVAKGAQIE 578
QY 266 AQ-----ARCRFPQKDEGGYFYFGELPLSLAACTNQPHIVN 302
Db 579 SSSDTKTVLHTAIFYGNESIVRYFIAGVTIDRRDEGKTAFD-----IAC----- 624
QY 303 YLTENPHKKADMRR---QDSRGNTVLHVAIAID-----NTRNTKF---VTMKYDLL 349
Db 625 ---ENDHK--DVARAFLETQWKNLIPCDVIPLDKHNPNVMKERTPFRLTKFPELA 679
QY 350 -----LLKCARLPDPSNLEAVLNNDGLSPLMAAKTGKIGIFQHIIR-REVTDTRHL 402
Db 680 SFVMDNCIEKSKETDSTQSVAVNFELDDTYMRCVSDDTGTEQLIGCKSAYDED---- 735
QY 403 SRKFKWAYGVPYSSLYDLSLDTCCGEASVLEILVYN-----SKIENRHEMLAVEPINE 457
Db 736 ---FLEKDAQSYASNVD-----RVYKHPLKLMADAELKH--LNLHPUSK 776
QY 458 -LLRDKWRKFGAVFYINVSYLCAWIFLTITAYYQLEGTPPYRTTVDYLRAGEVI 516
Db 777 ALLKXKNNLRGRPMYFALFWYL--VFIVSLTQVVRHTKA---PYNVWNEESYDS-- 828
QY 517 TLFQGVLPFFNTIKDLPMKCPGVNSLFD-----GSFOLLY----- 553
Db 829 -----YFDEN-----ETCPQINTTKPDVVMVKIIITQLAVCQILVECFQKFAYL 875
QY 554 -----FYSVLVIV---SAALYLAGIEAVLAVMVFALVL--GMMNALYFTRGKL 598
Db 876 VNWENWIDCFIYSTALITVVDVFECSATSGVRQWQWILAAALCFFGWINLLFMIRKMPR 935
QY 599 TGTYSIMQIKFLDFLLFLVLLFMIGYASALVSLNPNCAVMKVCNEDQNTCTVPTYP 658
Db 936 FGI FVVMFVDIV-KTFFRFPVFLFIIFSSSVFVL----- 972
QY 659 SCRDSFTSTFLDLFKLTGM-----GD-----LEMLSSTKYPVVFILLVTVI 703
Db 973 --QNRPEFTIFMSPLKTTVMVIGEFETGIFGHDETHAEKMFPAHTAVACALFFPFC 1030

664 DVEWK 668

RESULT 13
JH0588
calmodulin-binding protein trpl - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C:Accession: JH0588
R:Phillips, A.M.; Bull, A.; Kelly, L.E.
Neuron 8, 631-642, 1992
A:title: Identification of a Drosophila gene encoding a calmodulin-binding protein with 1
A:reference number: JH0588; MUID:92232293; PMID:1314616
A:Accession: JH0588
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1124 <PHI>
A:Cross-references: UNIPROT:P48994; GB:M88185; NID:9469057; PID:G158715
A:Experimental source: head
C:Genetics:
A:Gene: trpl
A:Cross-references: FlyBase:FBgn0005614
C:Superfamily: TRPC3 protein
C:Keywords: calmodulin binding; phosphoprotein; transmembrane protein
F:341-362/Domain: transmembrane #status predicted <TM1>
F:374-396/Domain: transmembrane #status predicted <TM2>
F:462-479/Domain: transmembrane #status predicted <TM3>
F:512-533/Domain: transmembrane #status predicted <TM4>
F:549-572/Domain: transmembrane #status predicted <TM5>
F:643-668/Domain: transmembrane #status predicted <TM6>
F:710-727,809-825/Region: calmodulin binding #status predicted
F:722/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 3.8%; Score 145.5; DB 2; Length 1124;
Best Local Similarity 19.3%; Pred. No. 0.057;
Matches 141; Conservative 99; Mismatches 237; Indels 253; Gaps 34;

QY 189 STGKTCPLKALLNLNSGNDTIPVLDD-----IAERTG---NMREFINSPFDIYR--- 237
DB 24 SVGGCCVPLGLQ-----PILLEKFFLAVERGDMENVRRILOKALRHQININC 74
QY 238 ----GOTALHIAIERRKHYVELLVAQCAD-----VHAQ 267
DB 75 MDPLGRRLTALADNENLEWVELLVVMGVETKDALLHAINAEFVEAVELLESLEIYKE 134
QY 268 ARGFPQKDEGGFYFYGEI-PLSLAAGTNOPIVNYITEN-----PH----- 309
DB 135 GEPYSQWQDVINTAMFADPTPLMLAAHKNNFEILILLDRGAAPVPVHDIRCGCECVR 194
QY 310 --KKADMRRODSRGN---TVLHALVAIADNTRETKE-----VTKM-----YDL 348
DB 195 LTAEDSLRLHSLSRVNIYALCSPSLICLTSDNPSTAFQLSWELRNLAUTEQECSEYMD 254
QY 349 LLLKCARLFPD-----SNLEAVLNDGSLPLMMAAKTGKIGIFQHIIRREVTDEDDR 400
DB 255 LRQCQKFAVDLLDQTRTSNELAILNV-----PQMSSVEPG-----DRM 295
QY 401 HLSRKFKDWAYGP-----VYSSLYDL-----SSLD--TCGEASV---LEI 436
DB 296 SLTRLVQAIISYKQKKFVAHNGNIQQLSSIWYDGLPGFRRKSIIVDKVICIAQAVLVFLPYC 355
QY 437 LVNYSKIENHEMLAVRPINELLRDKWRKFGAVSFYINVSVLCAMVIFTLTAYIQPLEG 496
DB 356 LITWCAPNCTGQLMRKPF-----MKFLIHASSVLFLLFILIVS----- 395
QY 497 TPYPYRTTYVDYLRLAG-----FIDSGFLLYFIYSVLVIVSAALYLAGE-----AYLAVMVF 533
DB 396 ----Q-RADDDFVRIFGITRMKKELAEQELRQGRQTPSKLELIVVMYVIGFVWEEVQEIF 450
QY 534 MKKCPGVNSL-----FIDSGFLLYFIYSVLVIVSAALYLAGE-----AYLAVMVF 580
DB 451 ----AVGKMSYLRNNWNIIDFLRNSLY--VSVNCLRFAFYIQOATEIARDPQWAYIPREKW 505

QY 581 -----ALVLGMNALYTRGLKLTGYSI-----MIQKILFK-----DLFRLLVLLLEMI 626
Db 506 HDFDQLTAEGFAAANVFAALKVHLFSINPHLGLOLSGRWIDIVKFFFIITLVLP 565
QY 627 GYASALVLLNPNCAKMKVCNEDQTNCTVPTVP-----SCRDSETSTFLDLDFK 675
Db 566 AFACGLNQLLWYFAAL-----EKSQYV--LPGGRADNGSHGDCMKWRFRG-----NLFE 614
QY 676 LT-----IGMGDLEMSSSTKYPVVF-IILLVTVIILTFVLLLNWLLMGMETVQ 724
Db 615 SSQSFLWASFGVGLDDFELSGIKSYTRFWGLMFGSYVINIVLLNLLIAMNSYAM 674
QY 725 VSKESKHIWK 734
Db 675 IDEHSDTEWK 684

RESULT 14
I38361
TRPC1 protein - human
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 04-Sep-1998
C:Accession: I38361
R:Wes, P.D.; Chevesich, J.; Jeromin, A.; Rosenberg, C.; Stetten, G.; Montell, C.
Proc. Natl. Acad. Sci. U.S.A. 92, 9652-9656, 1995
A:Title: TRPC1, a human homolog of a Drosophila store-operated channel.
A:Reference number: I38361; MUID:96003837; PMID:7568191
A:Accession: I38361
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-810 <RES>
A:Cross-references: EMBL:X89066; NID:g1019786; PID:g1019787
C:Superfamily: TRPC3 protein

Query Match 3.6%; Score 138.5; DB 2; Length 810;
Best Local Similarity 18.1%; Pred. No. 0.11;
Matches 147; Conservative 126; Mismatches 315; Indels 223; Gaps 36;
QY 12 PGEVAELPDGDESGTGGFAFLSSLANLFEDEGSLSPDASRPAGPGGRPNLRMKF 71
Db 3 PG-----IPGRAEAAGVTHPPFSPGAWLGSQSGS---GPVGAPPPS-----42
QY 72 QGAERKGVNPDLDLESTLYESSVVPVPGPKAPMDSLPDYGYVRHSSDNKRWRKILIEQ 131
Db 43 -----PGLPPSWAAMMALYSTDLSGASSSL-----70
QY 132 POSKPAPQPPPIKVFNRPIILFDIVSRGSTADLGLPFLTHKK---RLTDEEFREP 188
Db 71 PSSPSSSPNEVMALK-----DVREVKENTLNEKL-FLACDKGYVMVKILLEN 121
QY 189 STGK---TCLP-----KALLNLNNGRNTIPVLLD-----IAERTGNMREFINPFRDIY 235
Db 122 SSGDLINCVDLGRNAVITITENENLILQLLDYGCQKLMERIQNPE---YSTMDV- 177
QY 236 YRGOTALHIAIERCKHVVELLVAQADV---HA-QARGRFQPKDEGGYFVFGELPLSL 291
Db 178 -----APVILAHRNNYEILTMLLQDVSLPKPHAVGCECTCSAKNKKDSLHRFRFLDI 233
QY 292 AACTNQPHVNYLTENPHKKAMRRQDSRGNTVILHALVAIAD-----NTRENT 339
Db 234 YRCLASPALIMLTEDP-----ILRAPELSADLKLSLVEFRNDVEEL 278
QY 340 KFTVTKYDILLKLCARLPDPSNLEAVLNND-----GLSPMLMAKTGKI 383
Db 279 ARQCKMFAKDLLAQAAR--NSREVELINHTSSDBPLDKRGLERMMNLRLKLAIKYN-- 334
QY 384 GIFQHIIRREVTDETRHLSKFKDWAYCPVYSLSYDLSLDTCEEASVLEILVYNSKI 443
Db 335 -----QKEFVSQSN---COQFLNTW---FGQMSGYRKPCTCKIMTLVTGIF----- 377
QY 444 ENRHEMLAVEPINELLRDKWRKFGAV-----SFYINVVSYLCAMVIFTL-TAYYQPLE 496

Db 378 -----WPVLSLYLAPK-SQFGRIHTPMPKFIHGASYFTFLLLLNLXSLVYNEDKK 430
QY 497 TTPPYRTTVDYLRLAGEVITLFTGVLFNFKDLMKKCPGNSLFDIDSGFQLLYIYI 556
Db 431 NTMGPALERIDYL-----LILWIIIMI--WSDIKRLWYE--GLED-FLBERSNLQSFVM 479
QY 557 SVLTVSAALVLAG-----JEAYLAVMV-----PALVLGMNALYFTRGLKL 598
Db 480 NSLIATLAFALKVVAHNKHPDADRDKWDADFPTLVAEGLFAFANVLSYLRLEFFMTTSSI 539
QY 599 TGTYSIMIQIKLFDLFRFLAVYLLFMIGYASALVSLNPNCAKMKVCNEDQTNCTVPTYP 658
Db 540 LGPLQISMGQML-QDFGKFLGMFLLVLFSTFGLTQLYDKGYTSK-----EQKDC-VGIFC 593
QY 659 SCRDSSTFSTFLDLFLKLTIGMGDLEMSSSTKYPVVF-----ILLVTVI 703
Db 594 EQQSNDFTHSFIGTCFAL-----FWYIFSUAHVAIFVTRFSYGBELQSFVGAVIVGTYN 647
QY 704 ILTFVLLNLMLIALMGMETVGOVSKESKHIWK 734
Db 648 VVVIVLTKLLVAMLHKSFQLIANHEDKEWK 678

RESULT 15
T00894
hypothetical protein F21B7.8 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T00894
R:Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Conveologis, A.; Ecker, J.R.
submitted to the EMBL Data Library, January 1998
A:Description: Genomic sequence for Arabidopsis thaliana BAC F21B7.
A:Reference number: Z14208
A:Accession: T00894
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-616 <SHI>
A:Cross-references: UNIPROT:Q9LR59; EMBL:AC002560; NID:g2618677; PID:g2809239; GSPDB:GN0C
C:Genetics:
A:Gene: ATSP:F21B7.8
A:Map position: 1
A:Introns: 229/1; 411/3

Query Match 3.6%; Score 137; DB 2; Length 616;
Best Local Similarity 20.2%; Pred. No. 0.097;
Matches 123; Conservative 93; Mismatches 212; Indels 180; Gaps 30;
QY 161 GSTADLDGLLPFLTHKRLTDEEFREPSTGKTCLPKA--LLNLNNGRNDTIPVLLDIAE 218
Db 17 GSLSDPDQWTF-----KDKDESEIMNPAL--LCAVRAGDKVSLKLRINDDVKTQRLVD 69
QY 219 RTGN-----MREFINSPF-----RDIYRGOTALHIAIERCKHVVELLY--- 258
Db 70 NQGSILHIAAALGHVHIVEFIISTFENLLQNVLMGSETTLHVAARAGSLNIVEILVRFI 129
QY 259 -----AQGAD--VHAQAGR-----FFQPKDEGGYFY---283
Db 130 TESSYDAFTAASKGDBGTALHAALKGKHEVAFCLSVSKHDVSKDNDEASPLYMAVE 189
QY 284 --FCEPLSLAACNTQPHVNYLVE-----NPHKKADM-----ROD-----SRG 321
Db 190 AGYHELVLKMLESSSPSILLASMFSGKSVIHAAMKANRRDILGIVLRQDPGLIELNEEG 249
QY 322 NTVLHALVAIADNTRENTKFTVKYDLLLLKCARLPDPSNLEAVLNNDGLSPLMAAKTG 381
Db 250 RTCLS--YGASMGCEGIRVILAEFD---KAA-----SSLCYVADDDGFTPIHMAKEG 298
QY 382 KIGIFQHIIR-----REVTDERTH-----LSRKFKDWAY-----GPVYSSLYDLSS- 423
Db 299 HVRILKEFLKCHCPDSRELLNNQCONIFHVAIAAGSKVVKYLLKLDEGKRMNNQDINGN 358
QY 424 ----LDTGCEASVLEILVYNSKIENR---HEMLAVEPINELLRDKWRKFGAVSYINNV 476

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OM protein - protein search, using sw model

Run on: May 4, 2005, 22:04:33 ; Search time 83 Seconds
(without alignments)
4577.865 Million cell updates/sec

Title: US-10-090-215-12

Perfect score: 3858

Sequence: 1 MADSEGPAGGGEVAELPG.....GVSKSKHKLWQSGRRRL 742

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3829	99.2	853	2 Q86YZ6	Q86yz6 homo sapien
2	3829	99.2	871	2 Q8NDY7	Q8ndy7 homo sapien
3	3829	99.2	871	2 Q9GQ92	Q9gq92 homo sapien
4	3829	99.2	871	2 Q9HBC0	Q9hbc0 homo sapien
5	3828	99.2	871	2 Q9HBA0	Q9hba0 homo sapien
6	3695	95.8	871	2 Q9EPK8	Q9epk8 mus musculus
7	3693	95.7	871	2 Q9ERZ8	Q9erz8 rattus norv
8	3689	95.6	871	2 Q9ES76	Q9es76 mus musculus
9	3681	95.4	871	2 Q9EQZ4	Q9eqz4 mus musculus
10	3636	94.2	873	2 Q9ERZ7	Q9erz7 mus musculus
11	3472	90.0	803	2 Q9ERS7	Q9ers7 homo sapien
12	3466	89.8	811	2 Q9NG64	Q9ng64 homo sapien
13	3389	87.8	803	2 Q9LXR5	Q9lxr5 mus musculus
14	3284	85.1	852	2 Q9DFS3	Q9dfs3 gallus gall
15	1604.5	41.6	843	2 Q9CFN9	Q9cfn9 gallus gall
16	1603	41.6	839	2 Q9F5A3	Q9f5a3 cavia porce
17	1598.5	41.4	839	2 Q9KIW1	Q9kiw1 cavia porce
18	1580.5	41.0	838	2 Q9JMS7	Q9jms7 rattus norv
19	1580	41.0	839	2 Q704Y3	Q704y3 mus musculus
20	1579.5	40.9	838	2 Q35433	Q35433 rattus norv
21	1563	40.5	829	2 Q68SW0	Q68sw0 mus musculus
22	1557.5	40.4	839	2 Q8NER1	Q8ner1 homo sapien
23	1556.5	40.3	839	2 Q9NQ74	Q9nq74 homo sapien
24	1555.5	40.3	839	2 Q9NY22	Q9ny22 homo sapien
25	1552.5	40.2	842	2 Q9RX08	Q9rx08 oryctolagus
26	1551.5	40.2	839	2 Q9H0G9	Q9h0g9 homo sapien
27	1551.5	40.2	839	2 Q9H304	Q9h304 homo sapien
28	1547	40.1	840	2 Q697L1	Q697l1 canis famil
29	1369	35.5	778	2 Q9JMS6	Q9jms6 rattus norv
30	1324	34.3	761	2 Q9WUD2	Q9wud2 rattus norv
31	1322	34.3	761	2 Q9QYH8	Q9qyh8 rattus norv

32	1322	34.3	762	2 Q9JMI8	Q9jmi8 rattus norv
33	1321	34.2	791	2 Q8K424	Q8k424 mus musculus
34	1316	34.1	790	2 Q8NPH2	Q8nfh2 homo sapien
35	1312	34.0	790	2 Q8NDW7	Q8ndw7 homo sapien
36	1309	33.9	765	2 Q8NET9	Q8net9 homo sapien
37	1309	33.9	791	2 Q8NET8	Q8net8 homo sapien
38	1304.5	33.8	756	2 Q6JGX2	Q6jgx2 f-11 rat/mo
39	1304.5	33.8	756	2 Q9WTR1	Q9wtr1 mus musculus
40	1304.5	33.8	756	2 Q99K71	Q99k71 mus musculus
41	1298.5	33.7	764	2 Q9Y591	Q9y591 homo sapien
42	1287	33.4	764	2 Q9Y670	Q9y670 homo sapien
43	1071	27.8	511	2 Q9H303	Q9h303 homo sapien
44	1041	27.0	468	2 Q9Z0B4	Q9z0b4 rattus norv
45	1007.5	26.1	528	2 Q9Z182	Q9z182 rattus norv

ALIGNMENTS

RESULT 1

Q86YZ6					
ID	Q86YZ6	PRELIMINARY;	PRT;	853 AA.	
AC	Q86YZ6;				
DT	01-JUN-2003 (Tremblrel. 24, Created)				
DT	01-JUN-2003 (Tremblrel. 24, Last sequence update)				
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)				
DE	Hypothetical protein TRPV-SV.				
GN	Name=TRPV-SV;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Suzuki S.;				
RL	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Suzuki M.;				
RL	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AB100308; BACS5864.1; -				
DR	GO; GO:0016021; C:integral to membrane; IEA.				
DR	GO; GO:0005261; P:cation channel activity; IEA.				
DR	GO; GO:0006812; P:cation transport; IEA.				
DR	InterPro; IPR002110; ANK.				
DR	InterPro; IPR002111; Cat_channel_TrpL.				
DR	InterPro; IPR005821; Ion_trans.				
DR	InterPro; IPR004729; TRPChannel.				
DR	InterPro; IPR008347; Vanil_receptor.				
DR	InterPro; IPR008348; Vanil_receptor2.				
DR	Pfam; PF00023; Ank; 3.				
DR	Pfam; PF00520; Ion_trans; 1.				
DR	PRINTS; PR01415; ANKYRIN.				
DR	PRINTS; PR01768; TRPVRECEPTOR.				
DR	PRINTS; PR01769; VRL2RECEPTOR.				
DR	SMART; SM00248; ANK; 3.				
DR	TIGRFAMS; TIGR00870; ttp; 1.				
DR	PROSITE; PS50088; ANK_REPEAT; 1.				
DR	PROSITE; PS50297; ANK_REPEAT_REGION; 1.				
KW	ANK repeat; Hypothetical protein; Ion transport; Ionic channel;				
KW	Transmembrane; Transport.				
SQ	SEQUENCE 853 AA; 96448 MW; EAA07196606AED20 CRC64;				

Query Match	99.2%;	Score 3829;	DB 2;	Length 853;
Best Local Similarity	100.0%;	Pred. No. 1.4e-231;		
Matches 736;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MADSEGPAGGGEVAELPGDESGTTPGGEAFPLSSLANLFEDEGSLSPSPADASRPAGP	60	
Db	1	MADSEGPAGGGEVAELPGDESGTTPGGEAFPLSSLANLFEDEGSLSPSPADASRPAGP	60	
QY	61	GDGPNLKMFKQGAFRKGVNPDILLETLYESSVVPQPKAPMDSLDYGYRHHSSN	120	

Db 61 GDRPNLRMKFOGAFKGVNPIDILLESITYESSVVPKAPMDSLFDYGYRHHSSDN 120
QY 121 KWRKKIIEKQSPKAPAPPPILKVNRPILFDIVSRGSTDGLPFLTHKKRL 180
Db 121 KWRKKIIEKQSPKAPAPPPILKVNRPILFDIVSRGSTDGLPFLTHKKRL 180
QY 181 TDEEREPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFFINSFRDIYRGQT 240
Db 181 TDEEREPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFFINSFRDIYRGQT 240
QY 241 ALHIAIERRCKHYVELLVAAQADVHAQARGFPQKDEGGYFYGELPLSLAACTNQPHI 300
Db 241 ALHIAIERRCKHYVELLVAAQADVHAQARGFPQKDEGGYFYGELPLSLAACTNQPHI 300
QY 301 VNYLTENPHKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKCARLFPDS 360
Db 301 VNYLTENPHKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKCARLFPDS 360
QY 361 NLEAVLNNDGLSPLMMAAKTGKIGIFOHIIRREVTDTRHLRSRKFCDWAYGVPVSSLYD 420
Db 361 NLEAVLNNDGLSPLMMAAKTGKIGIFOHIIRREVTDTRHLRSRKFCDWAYGVPVSSLYD 420
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINNVSYLC 480
Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINNVSYLC 480
QY 481 AMVITLTAYQPLEGTPPYRRTVDYLRAGEVITLFTGVLPFTTNIKOLFMMKCCPGV 540
Db 481 AMVITLTAYQPLEGTPPYRRTVDYLRAGEVITLFTGVLPFTTNIKOLFMMKCCPGV 540
QY 541 NSLFDGSGFOLLFYIYSVLVISAALYAGIAYLAVMVFAVLGWMNALYFTGLKLTG 600
Db 541 NSLFDGSGFOLLFYIYSVLVISAALYAGIAYLAVMVFAVLGWMNALYFTGLKLTG 600
QY 601 TYSIMIQILFKDLFRLLVLLFMIGYASALVSLNPNCAKMKVCNEQTNCTVPTPSC 660
Db 601 TYSIMIQILFKDLFRLLVLLFMIGYASALVSLNPNCAKMKVCNEQTNCTVPTPSC 660
QY 661 RDETFSTFLDLFKLTGMGDMLEMLSTKYPVFIILLVYIILTVLLNMLIALMGE 720
Db 661 RDETFSTFLDLFKLTGMGDMLEMLSTKYPVFIILLVYIILTVLLNMLIALMGE 720
QY 721 TVGQVSKESKHIWKLO 736
Db 721 TVGQVSKESKHIWKLO 736

RESULT 2
QBNDY7 PRELIMINARY; PRT; 871 AA.
AC QBNDY7
ID QBNDY7
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Vanilloid receptor-like channel 2.
GN Name=VRL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2107054; PubMed=12077606; DOI=10.1038/nature00894;
RA Smith G.D.; Gunthorpe M.J.; Kelsell R.E.; Hayes P.D.; Reilly P.;
RA Facer P.; Wright J.E.; Jerman J.C.; Wallin J.-P.; Ooi L.; Egerton J.;
RA Charles K.J.; Smart D.; Randall A.D.; Anand P.; Davis J.B.;
RT "TRPV3 is a temperature-sensitive vanilloid receptor-like protein.";
RL Nature 418:186-190(2002).
DR EMBL; AJ296305; CAC82937.1; --
DR Genbank; HGNC:18083; TRPV4.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR004729; TrpChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR InterPro; IPR008348; Vanil_receptor2.
DR Pfam; PF00023; Ank; 3.
DR Pfam; PF00520; Ion trans; 1.
DR PRINTS; PRO1415; ANKYRIN.
DR PRINTS; PRO1768; TRPVRECEPTOR.
DR PRINTS; PRO1769; VRL2RECEPTOR.
DR SMART; SM00248; ANK; 3.
DR TIGRFAMs; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT; 1.
KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW Transport.
SQ SEQUENCE 871 AA; 98280 MW; C62056B86C5A6FB6 CRC64;
Query Match 99.2%; Score 3829; DB 2; Length 871;
Best Local Similarity 100.0%; Pred. No. 1.4e-231;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MADSEGPAGCGEVAELPGDESGTGCGEATPLSSLANLFEDEGSLSPSADASRRPAG 60
Db 1 MADSEGPAGCGEVAELPGDESGTGCGEATPLSSLANLFEDEGSLSPSADASRRPAG 60
QY 61 GDGRPNLRMKFOGAFKGVNPIDILLESITYESSVVPKAPMDSLFDYGYRHHSSDN 120
Db 61 GDGRPNLRMKFOGAFKGVNPIDILLESITYESSVVPKAPMDSLFDYGYRHHSSDN 120
QY 121 KWRKKIIEKQSPKAPAPPPILKVNRPILFDIVSRGSTDGLPFLTHKKRL 180
Db 121 KWRKKIIEKQSPKAPAPPPILKVNRPILFDIVSRGSTDGLPFLTHKKRL 180
QY 181 TDEEREPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFFINSFRDIYRGQT 240
Db 181 TDEEREPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFFINSFRDIYRGQT 240
QY 241 ALHIAIERRCKHYVELLVAAQADVHAQARGFPQKDEGGYFYGELPLSLAACTNQPHI 300
Db 241 ALHIAIERRCKHYVELLVAAQADVHAQARGFPQKDEGGYFYGELPLSLAACTNQPHI 300
QY 301 VNYLTENPHKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKCARLFPDS 360
Db 301 VNYLTENPHKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKCARLFPDS 360
QY 361 NLEAVLNNDGLSPLMMAAKTGKIGIFOHIIRREVTDTRHLRSRKFCDWAYGVPVSSLYD 420
Db 361 NLEAVLNNDGLSPLMMAAKTGKIGIFOHIIRREVTDTRHLRSRKFCDWAYGVPVSSLYD 420
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINNVSYLC 480
Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINNVSYLC 480
QY 481 AMVITLTAYQPLEGTPPYRRTVDYLRAGEVITLFTGVLPFTTNIKOLFMMKCCPGV 540
Db 481 AMVITLTAYQPLEGTPPYRRTVDYLRAGEVITLFTGVLPFTTNIKOLFMMKCCPGV 540
QY 541 NSLFDGSGFOLLFYIYSVLVISAALYAGIAYLAVMVFAVLGWMNALYFTGLKLTG 600
Db 541 NSLFDGSGFOLLFYIYSVLVISAALYAGIAYLAVMVFAVLGWMNALYFTGLKLTG 600
QY 601 TYSIMIQILFKDLFRLLVLLFMIGYASALVSLNPNCAKMKVCNEQTNCTVPTPSC 660
Db 601 TYSIMIQILFKDLFRLLVLLFMIGYASALVSLNPNCAKMKVCNEQTNCTVPTPSC 660
QY 661 RDETFSTFLDLFKLTGMGDMLEMLSTKYPVFIILLVYIILTVLLNMLIALMGE 720
Db 661 RDETFSTFLDLFKLTGMGDMLEMLSTKYPVFIILLVYIILTVLLNMLIALMGE 720
QY 721 TVGQVSKESKHIWKLO 736

Qy	361	NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDTRHLRSRKFQKWAYGVPVSSLYD	420
Db	361	NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDTRHLRSRKFQKWAYGVPVSSLYD	420
Qy	421	LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINEILLRDKWRKEGAVSFYINNVSYLC	480
Db	421	LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINEILLRDKWRKEGAVSFYINNVSYLC	480
Qy	481	AMWIFTLTAYYQPLEGTPPYRTTVDYLRAGEVITLTFTGLVFFFTNIKDLFMKKCPGV	540
Db	481	AMWIFTLTAYYQPLEGTPPYRTTVDYLRAGEVITLTFTGLVFFFTNIKDLFMKKCPGV	540
Qy	541	NSLFDGSQLLYFYISVLYVSAALYLAGIEAYLAVMVFAVLVGMWALYFTRGLKLTG	600
Db	541	NSLFDGSQLLYFYISVLYVSAALYLAGIEAYLAVMVFAVLVGMWALYFTRGLKLTG	600
Qy	601	TYSIMIQKILFKDLFRFLVLLFMIGYASALVSLNFCANMKVCNEDQTNCTVPTPSC	660
Db	601	TYSIMIQKILFKDLFRFLVLLFMIGYASALVSLNFCANMKVCNEDQTNCTVPTPSC	660
Qy	661	RDSETFTFLDLPLKLTIGMGDLEMLSTKYPVVFIIILLVTYIIITFVLLNMLALMGE	720
Db	661	RDSETFTFLDLPLKLTIGMGDLEMLSTKYPVVFIIILLVTYIIITFVLLNMLALMGE	720
Qy	721	TVGQVSKESKHIWKIQ 736	
Db	721	TVGQVSKESKHIWKIQ 736	
RESULT 4			
Q9HBC0		PRELIMINARY; PRT; 871 AA.	
ID	Q9HBC0		
AC	Q9HBC0;		
DT	01-MAR-2001 (TREMBlrel. 16, Created)		
DT	01-MAR-2001 (TREMBlrel. 16, Last sequence update)		
DT	01-MAR-2004 (TREMBlrel. 26, Last annotation update)		
DE	OTRPC4.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Renal cortex;		
RX	MEDLINE=20482174; PubMed=11025659; DOI=10.1038/35036318;		
RA	Strotmann R., Harteneck C., Nunnenmacher K., Schultz G., Plant T.D.;		
RT	"OTRPC4, a nonselective cation channel that confers sensitivity to extracellular osmolarity."		
RL	Nat. Cell Biol. 2:695-702(2000).		
DR	EMBL; AF258465; AAG16127.1; -		
DR	GO; GO:0016021; C:integral to membrane; NAS.		
DR	GO; GO:0015281; F:nonselective cation channel activity; NAS.		
DR	GO; GO:0006816; P:calcium ion transport; NAS.		
DR	InterPro; IPR002110; ANK.		
DR	InterPro; IPR002111; Cat channel_TrpL.		
DR	InterPro; IPR005821; Ion_trans.		
DR	InterPro; IPR004729; TRPChannel.		
DR	InterPro; IPR008347; Vanil_receptor.		
DR	InterPro; IPR008348; Vanil_receptor2.		
DR	Pfam; PF00023; Ank; 3.		
DR	Pfam; PF00520; Ion_trans; 1.		
DR	PRINTS; PR01415; ANKYRIN.		
DR	PRINTS; PR01768; TRPVRECEPTOR.		
DR	PRINTS; PR01769; VRL2RECEPTOR.		
DR	SMART; SM00248; ANK; 3.		
DR	TIGRFAMS; TIGR00870; trp; 1.		
DR	PROSITE; PS00088; ANK_REPEAT; 1.		
DR	PROSITE; PS00297; ANK_REPEAT_REGION; 1.		
KW	ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane; Transport.		
SK	SEQUENCE 871 AA; 98294 MW; C62056B86DEA6FB6 CRC64;		
Query Match 99.2%; Score 3829; DB 2; Length 871;			
Best Local Similarity 100.0%; Pred. No. 1.4e-231;			
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	MADSEGPAGGVAELPGDESGTPGGEAFPLSLANLFEDEGSLSPSPADASRPAGP 60	
Db	1	MADSEGPAGGVAELPGDESGTPGGEAFPLSLANLFEDEGSLSPSPADASRPAGP 60	
Qy	61	GDGRNLRMKTQGAQKGVNPNIDLESTLYESSVVPQKAPMDSLFDYGYRHHSSDN 120	
Db	61	GDGRNLRMKTQGAQKGVNPNIDLESTLYESSVVPQKAPMDSLFDYGYRHHSSDN 120	
Qy	121	KWRKRIIEKQPSKAPAPQPPILKVFNRPIILFDIVSRGSTADLDGLLPFLTHKKRL 180	
Db	121	KWRKRIIEKQPSKAPAPQPPILKVFNRPIILFDIVSRGSTADLDGLLPFLTHKKRL 180	
Qy	181	TDEEFREPSTGKTCPLKALLNSGRNTIPVLLDIAERTGNMREFINSPFDIYRGQT 240	
Db	181	TDEEFREPSTGKTCPLKALLNSGRNTIPVLLDIAERTGNMREFINSPFDIYRGQT 240	
Qy	241	ALHTAIERCKHYVELLVAQAGADVAHQARFPQPKDEGGYFYFGELPLSLAACTNQPHI 300	
Db	241	ALHTAIERCKHYVELLVAQAGADVAHQARFPQPKDEGGYFYFGELPLSLAACTNQPHI 300	
Qy	301	VNYLTENPHKKADMRQDSRGNTVLHALVAADNTRENTKFTQYDILLKLCARLFPDS 360	
Db	301	VNYLTENPHKKADMRQDSRGNTVLHALVAADNTRENTKFTQYDILLKLCARLFPDS 360	
Query Match 99.2%; Score 3829; DB 2; Length 871;			
Best Local Similarity 100.0%; Pred. No. 1.4e-231;			

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Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MADSEGPAGGVAELPGDESGTGGGAAPLSSLANLFEDEGSLSPSPADASRPAGP 60
DB 1 MADSEGPAGGVAELPGDESGTGGGAAPLSSLANLFEDEGSLSPSPADASRPAGP 60
QY 61 GDGRPNLRMKFQAGFRKGVNPIDILLESSTLYESSVVPKAPMDSLFYGYRHHSDN 120
DB 61 GDGRPNLRMKFQAGFRKGVNPIDILLESSTLYESSVVPKAPMDSLFYGYRHHSDN 120
QY 121 KWRKKIIEKQPSKAPAPQPPILKVFNRPIFLDIVSRGSTDLDGLLPFLTHKKRL 180
DB 121 KWRKKIIEKQPSKAPAPQPPILKVFNRPIFLDIVSRGSTDLDGLLPFLTHKKRL 180
QY 181 TDEFRPSTGKTCLPKALLNSGRNDTIPVLLDIAERTGNMREFFINSFRDIYYRGT 240
DB 181 TDEFRPSTGKTCLPKALLNSGRNDTIPVLLDIAERTGNMREFFINSFRDIYYRGT 240
QY 241 ALHIAIERCKHYVELLVQAQADVHAQARGFPQKDEGGYFYGELPLSLAACTNQPHI 300
DB 241 ALHIAIERCKHYVELLVQAQADVHAQARGFPQKDEGGYFYGELPLSLAACTNQPHI 300
QY 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKLCARLPDS 360
DB 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKLCARLPDS 360
QY 361 NLEAVLNNDGLSPLMAAKTKIGIFQHIIRREVTDTRHLSRKFKDWAYGPVYSSLYD 420
DB 361 NLEAVLNNDGLSPLMAAKTKIGIFQHIIRREVTDTRHLSRKFKDWAYGPVYSSLYD 420
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYINNVSYLC 480
DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYINNVSYLC 480
QY 481 AMVIFTLTAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFFFTNIKDFMKKCPGV 540
DB 481 AMVIFTLTAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFFFTNIKDFMKKCPGV 540
QY 541 NSLFDGFSQLLYFYISVIVSAALYLAGIAYLVAVFALVGLGWNALYFTGLKLTG 600
DB 541 NSLFDGFSQLLYFYISVIVSAALYLAGIAYLVAVFALVGLGWNALYFTGLKLTG 600
QY 601 TYSIMIQKILFKDLFRLLVYLLFMIGYASALVSLNPNCAKMKVCNEQDQNTCTVTPSPC 660
DB 601 TYSIMIQKILFKDLFRLLVYLLFMIGYASALVSLNPNCAKMKVCNEQDQNTCTVTPSPC 660
QY 661 RDSEFTFTLLDLFKLTIGMGDLEMLSTKYPVVFILLVTVIILTFVLLNMLIALMGE 720
DB 661 RDSEFTFTLLDLFKLTIGMGDLEMLSTKYPVVFILLVTVIILTFVLLNMLIALMGE 720
QY 721 TVGVQSKESKHIWKLO 736
DB 721 TVGVQSKESKHIWKLO 736
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RESULT 5

```
Q9HBA0 PRELIMINARY; PRT; 871 AA.
AC Q9HBA0
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Vanilloid receptor-related osmotically activated channel.
GN Name=VROAC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20531888; PubMed=11081638; DOI=10.1016/S0092-8674(00)00143-4;
RA Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,
RA Sali A., Hudepeth A.J., Friedman J.M., Heller S.;
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RT "Vanilloid receptor-related osmotically activated channel (VR-OAC), a
RT candidate vertebrate osmoreceptor.";
RL Cell 103:525-535(2000).
DR EMBL, AF263523; AAG28029.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat channel_Trlp.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR004729; TRPChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR InterPro; IPR008348; Vanil_receptor2.
DR Pfam; PF00023; Ank; 3.
DR PRINTS; PR01415; ANKVRIN.
DR PRINTS; PR01768; TRPVRECEPTOR.
DR PRINTS; PR01769; VRL2RECEPTOR.
DR SMART; SM00248; ANK; 3.
DR TIGRFAMS; TIGR00870; trp; 1.
DR PROSITE; PS0088; ANK_REPEAT; 1.
DR PROSITE; PS0297; ANK_REPEAT; 1.
KW ANK repeat; ion transport; ionic channel; Receptor; Transmembrane;
KW Transport.
SQ SEQUENCE 871 AA; 98265 MW; A86FB6ECC9103C19 CRC64;
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Query Match 99.2%; Score 3828; DB 2; Length 871;
Best Local Similarity 99.9%; Pred. No. 1.6e-231;
Matches 735; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MADSEGPAGGVAELPGDESGTGGGAAPLSSLANLFEDEGSLSPSPADASRPAGP 60
DB 1 MADSEGPAGGVAELPGDESGTGGGAAPLSSLANLFEDEGSLSPSPADASRPAGP 60
QY 61 GDGRPNLRMKFQAGFRKGVNPIDILLESSTLYESSVVPKAPMDSLFYGYRHHSDN 120
DB 61 GDGRPNLRMKFQAGFRKGVNPIDILLESSTLYESSVVPKAPMDSLFYGYRHHSDN 120
QY 121 KWRKKIIEKQPSKAPAPQPPILKVFNRPIFLDIVSRGSTDLDGLLPFLTHKKRL 180
DB 121 KWRKKIIEKQPSKAPAPQPPILKVFNRPIFLDIVSRGSTDLDGLLPFLTHKKRL 180
QY 181 TDEFRPSTGKTCLPKALLNSGRNDTIPVLLDIAERTGNMREFFINSFRDIYYRGT 240
DB 181 TDEFRPSTGKTCLPKALLNSGRNDTIPVLLDIAERTGNMREFFINSFRDIYYRGT 240
QY 241 ALHIAIERCKHYVELLVQAQADVHAQARGFPQKDEGGYFYGELPLSLAACTNQPHI 300
DB 241 ALHIAIERCKHYVELLVQAQADVHAQARGFPQKDEGGYFYGELPLSLAACTNQPHI 300
QY 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKLCARLPDS 360
DB 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKLCARLPDS 360
QY 361 NLEAVLNNDGLSPLMAAKTKIGIFQHIIRREVTDTRHLSRKFKDWAYGPVYSSLYD 420
DB 361 NLEAVLNNDGLSPLMAAKTKIGIFQHIIRREVTDTRHLSRKFKDWAYGPVYSSLYD 420
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYINNVSYLC 480
DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYINNVSYLC 480
QY 481 AMVIFTLTAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFFFTNIKDFMKKCPGV 540
DB 481 AMVIFTLTAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFFFTNIKDFMKKCPGV 540
QY 541 NSLFDGFSQLLYFYISVIVSAALYLAGIAYLVAVFALVGLGWNALYFTGLKLTG 600
DB 541 NSLFDGFSQLLYFYISVIVSAALYLAGIAYLVAVFALVGLGWNALYFTGLKLTG 600
QY 601 TYSIMIQKILFKDLFRLLVYLLFMIGYASALVSLNPNCAKMKVCNEQDQNTCTVTPSPC 660
DB 601 TYSIMIQKILFKDLFRLLVYLLFMIGYASALVSLNPNCAKMKVCNEQDQNTCTVTPSPC 660
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Db 601 TYSIMIQILFKDLFRFLVLLFMIGVASALVSLNFCANMKVCNEDQTNCTVTPYFSC 660
QY 661 RDSFTSFLLDLFKLTIGMGDLEMLSTKYPVPIILLVTVIITFVLLNMLALMGE 720
Db 661 RDSFTSFLLDLFKLTIGMGDLEMLSTKYPVPIILLVTVIITFVLLNMLALMGE 720
QY 721 TVGVQSKESKHIWKLO 736
Db 721 TVGVQSKESKHIWKLO 736

RESULT 6
Q9EPK8 PRELIMINARY; PRT; 871 AA.
ID Q9EPK8;
AC Q9EPK8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transient receptor potential protein 12.
GN Name=Trpv4; Synonyms=Trp12;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=20547522; PubMed=11094154; DOI=10.1016/S0014-5793(00)02212-2;
RA Wissenbach U., Boedding M., Freichel M., Flockerzi V.;
RT "Trp12, a novel Trp related protein from kidney.";
RL FEBS Lett. 485:127-134(2000).
DR EMBL; AJ296078; CAC20703.1; -.
DR MGD; MGI:1926945; Trpv4.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005262; F:calcium channel activity; IDA.
DR GO; GO:0005034; F:osmosensor activity; IDA.
DR GO; GO:0042538; P:hypersmotic salinity response; IMP.
DR GO; GO:0007231; P:osmosensory signaling pathway; IDA.
DR GO; GO:0047484; P:regulation of response to osmotic stress; IMP.
DR GO; GO:0030103; P:vasopressin secretion; IMP.
DR InterPro; IPR002110; Cat.
DR InterPro; IPR002111; Cat channel_TrpL.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR004729; TRPChannel.
DR InterPro; IPR008347; Vanil receptor.
DR InterPro; IPR008348; vanil_receptor2.
DR Pfam; PF00023; Ank; 3.
DR Pfam; PF00520; Ion trans; 1.
DR PRINTS; PR01768; TRPVRECEPTOR.
DR PRINTS; PR01769; VRL2RECEPTOR.
DR SMART; SM00248; ANK; 3.
DR TIGRFAMs; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK REPEAT; 1.
DR PROSITE; PS50297; ANK REP REGION; 1.
KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW Transport.
SQ SEQUENCE 871 AA; 98026 MW; 5BAC6E33F89CEA05 CRC64;

Query Match 95.8%; Score 3695; DB 2; Length 871;
Best Local Similarity 95.7%; Pred. No. 3.5e-223;
Matches 704; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 1 MADSEGRAGGEVAELPGDESGTGGGAFFPLSSLANLFEDEGSLSPSPADASRPAGP 60
Db 1 MADPGDGRAAPGEVAEPDGESEGTGGGAFFPLSSLANLFEDEGSSLSPPVDASRPAGP 60

QY 61 GDGRNLRMKFOCARKGVNPDILLESTLYESSVVPKAPMDSLFDYGYRHHSSDN 120
Db 61 GDGRNLRMKFOCARKGVNPDILLESTLYESSVVPKAPMDSLFDYGYRHHPSDN 120

QY 121 KWRKKIIEKQSPKAPAPQPPPIKLVNRPILFDIVSRGSTADLGLLPFLTHKKRL 180
Db 121 KWRKKVVEKQSPKAPAPQPPPIKLVNRPILFDIVSRGSTADLGLLSFLTHKKRL 180
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QY 181 TDEFPREPSTGKTCIPKALLNLSNGRNDTI PVLLDIAERTGNMREFINSPPFDIYYRGOT 240
Db 181 TDEFPREPSTGKTCIPKALLNLSNGRNDTI PVLLDIAERTGNMREFINSPPFDIYYRGOT 240
QY 241 ALHIAIERCKHYVELLVAQGADVHAQARGRFQPKDEGGYFYFGELPLSLAACTNQPHI 300
Db 241 SLHIAIERCKHYVELLVAQGADVHAQARGRFQPKDEGGYFYFGELPLSLAACTNQPHI 300
QY 301 VNYLTENPHKADMRQDSRGNTVHLAVALADNTRENTKFTVMYDILLLLLCARLPDPS 360
Db 301 VNYLTENPHKADMRQDSRGNTVHLAVALADNTRENTKFTVMYDILLLLLCARLPDPS 360
QY 361 NLEAVLNNDGLSPLMMAAKTKIGIFQHIIRREVTDTRHLSRKFQDWAYGVPVSSLYD 420
Db 361 NLEAVLNNDGLSPLMMAAKTKIGIFQHIIRREVTDTRHLSRKFQDWAYGVPVSSLYD 420
QY 421 LSSLDTCGEEASVLEILVNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
Db 421 LSSLDTCGEEVSVLEILVNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
QY 481 AMVIFTLTAYYQPLEGTPPYRTTVDYLRAGEVITLFTGVLPFTNFKDLFMKCPGV 540
Db 481 AMVIFTLTAYYQPLEGTPPYRTTVDYLRAGEVITLFTGVLPFTNFKDLFMKCPGV 540
QY 541 NSLFIDGSGFQLLYFTYSVLVIVSAALYLAGIEAYLAVMVFAVLGMMNALYFTRGLKLTG 600
Db 541 NSLVFDGSGFQLLYFTYSVLVIVSAALYLAGIEAYLAVMVFAVLGMMNALYFTRGLKLTG 600
QY 601 TYSIMIQILFKDLFRFLVLLFMIGVASALVSLNFCANMKVCNEDQTNCTVTPYFSC 660
Db 601 TYSIMIQILFKDLFRFLVLLFMIGVASALVSLNFCANMKVCNEDQTNCTVTPYFSC 660
QY 661 RDSFTSFLLDLFKLTIGMGDLEMLSTKYPVPIILLVTVIITFVLLNMLALMGE 720
Db 661 RDSFTSFLLDLFKLTIGMGDLEMLSTKYPVPIILLVTVIITFVLLNMLALMGE 720
QY 721 TVGVQSKESKHIWKLO 736
Db 721 TVGVQSKESKHIWKLO 736

RESULT 7
Q9ERZ8 PRELIMINARY; PRT; 871 AA.
ID Q9ERZ8;
AC Q9ERZ8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Vanilloid receptor-related osmotically activated channel.
GN Name=Vroac;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=20531888; PubMed=11081638; DOI=10.1016/S0092-8674(00)00143-4;
RA Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,
RA Sali A., Huidspeth A.J., Friedman J.M., Heller S.;
RT "Vanilloid receptor-related osmotically activated channel (VR-OAC), a
RL Cell 103:525-535(2000).
DR EMBL; AF263521; AAG28027.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat channel_TrpL.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR004729; TRPChannel.
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DR InterPro; IPR008347; Vanil receptor.
DR InterPro; IPR008348; Vanil_receptor2.
DR Pfam; PF00023; Ank; 3.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR01768; TRPVRECEPTOR.
DR PRINTS; PR01769; VRL2RECEPTOR.
DR SMART; SM00248; ANK; 3.
DR TIGRFAMs; TIGR00870; ttp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW Transport.
SQ SEQUENCE 871 AA; 98009 MW; 5D50684DA08C354B CRC64;

Query Match 95.7%; Score 3693; DB 2; Length 871;
Best Local Similarity 95.5%; Pred. No. 4.7e-223;
Matches 703; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

QY 1 MADSEGPRAAGPGEVAELPGDESGTGGGEAFPLSSLANLFEDEGSLSPADASRRPAGP 60
DB 1 MADPGDGPRAAPGDVAEPDDESGTSGGEAFPLSSLANLFEDEGSSLSLSPVDASRRPAGP 60

QY 61 GDGRPNLRMKFGQAFRGKGVNPIDLLSTLYESSVVPKAPMDSLFYGYRHHSSDN 120
DB 61 GDGRPNLRMKFGQAFRGKGVNPIDLLSTLYESSVVPKAPMDSLFYGYRHHSSDN 120

QY 121 KWRKKIIEKQPSKAPAPQPPPIKVFNPILFDIVSRGSTADLDGLLPFLTHKKRL 180
DB 121 KWRKKIIEKQPSKAPAPQPPPIKVFNPILFDIVSRGSTADLDGLLPFLTHKKRL 180

QY 181 TDEFPSTGKTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGQT 240
DB 181 TDEFPSTGKTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGQT 240

QY 241 ALHIAIERCKHYVELLVQAQADVHAQARGFPQKDEGGYFYGELPLSLAACTNQPHI 300
DB 241 ALHIAIERCKHYVELLVQAQADVHAQARGFPQKDEGGYFYGELPLSLAACTNQPHI 300

QY 241 ALHIAIERCKHYVELLVQAQADVHAQARGFPQKDEGGYFYGELPLSLAACTNQPHI 300
DB 241 ALHIAIERCKHYVELLVQAQADVHAQARGFPQKDEGGYFYGELPLSLAACTNQPHI 300

QY 301 VNYLTENPHKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKLCARLPDS 360
DB 301 VNYLTENPHKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKLCARLPDS 360

QY 361 NLEAVLNNDGLSPLMMAAKTKIGIFONHIIIRREVTDETRHLRKFQDWAYGPVYSSLYD 420
DB 361 NLEAVLNNDGLSPLMMAAKTKIGIFONHIIIRREVTDETRHLRKFQDWAYGPVYSSLYD 420

QY 421 LSSLLTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYINVSYLC 480
DB 421 LSSLLTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYINVSYLC 480

QY 481 AMVIFTLTAYQPLEGTPPYPRVTVDYLRLAGEVITLTGVLFFFTNIKDLFMKKCPGV 540
DB 481 AMVIFTLTAYQPLEGTPPYPRVTVDYLRLAGEVITLTGVLFFFTNIKDLFMKKCPGV 540

QY 541 NSLFDGSGFQLLYFYISVLVISAALYAGIAYLAVNVFALVLGWNALYFTGLKLTG 600
DB 541 NSLFDGSGFQLLYFYISVLVISAALYAGIAYLAVNVFALVLGWNALYFTGLKLTG 600

QY 601 TVSIMIQILFKDLFRLLVLLFMIGYASALVSLNFCANNKVCNEDOTNCTVPTVESC 660
DB 601 TVSIMIQILFKDLFRLLVLLFMIGYASALVSLNFCANNKVCNEDOTNCTVPTVESC 660

QY 661 RDSFTSFLLDLFKLTIGMGDLEMLSSTKYPVVFILLVYIILTFLVLLNMLIALMGE 720
DB 661 RDSFTSFLLDLFKLTIGMGDLEMLSSTKYPVVFILLVYIILTFLVLLNMLIALMGE 720

QY 721 TVGVQSKESKHIWKLO 736
DB 721 TVGVQSKESKHIWKLO 736
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ID Q9ES76 PRELIMINARY; PRT; 871 AA.
AC Q9ES76;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE OTRPC4 cation channel.
GN Name=Trpv4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvEv;
RA MEDLINE=20482174; PubMed=11025659; DOI=10.1038/35036318;
RA Stromann R., Harteneck C., Nuenenmacher K., Schultz G., Plant T.D.;
RT "OTRPC4, a nonselective cation channel that confers sensitivity to
RT extracellular osmolarity.";
RL Nat. Cell Biol. 2:695-702(2000).
DR EMBL; AF208026; AAG17543.1; -.
DR MGD; MGI:1928945; Trpv4.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005262; F:calcium channel activity; IDA.
DR GO; GO:0005034; F:osmosensor activity; IDA.
DR GO; GO:0042538; P:hyperosmotic salinity response; IMP.
DR GO; GO:0007231; P:osmosensory signaling pathway; IDA.
DR GO; GO:0047484; P:regulation of response to osmotic stress; IMP.
DR GO; GO:0030103; P:vasopressin secretion; IMP.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat channel_TripL.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR004729; TrpChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR InterPro; IPR008348; Vanil_receptor2.
DR Pfam; PF00023; Ank; 3.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR01768; TRPVRECEPTOR.
DR PRINTS; PR01769; VRL2RECEPTOR.
DR SMART; SM00248; ANK; 3.
DR TIGRFAMs; TIGR00870; ttp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 871 AA; 98069 MW; 2B228D554083F00A CRC64;
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Query Match 95.6%; Score 3689; DB 2; Length 871;
Best Local Similarity 95.5%; Pred. No. 8.4e-223;
Matches 703; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

QY 1 MADSEGPRAAGPGEVAELPGDESGTGGGEAFPLSSLANLFEDEGSLSPADASRRPAGP 60
DB 1 MADPGDGPRAAPGDVAEPDDESGTSGGEAFPLSSLANLFEDEGSSLSLSPVDASRRPAGP 60

QY 61 GDGRPNLRMKFGQAFRGKGVNPIDLLSTLYESSVVPKAPMDSLFYGYRHHSSDN 120
DB 61 GDGRPNLRMKFGQAFRGKGVNPIDLLSTLYESSVVPKAPMDSLFYGYRHHSSDN 120

QY 121 KWRKKIIEKQPSKAPAPQPPPIKVFNPILFDIVSRGSTADLDGLLPFLTHKKRL 180
DB 121 KWRKKIIEKQPSKAPAPQPPPIKVFNPILFDIVSRGSTADLDGLLPFLTHKKRL 180

QY 181 TDEFPSTGKTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGQT 240
DB 181 TDEFPSTGKTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGQT 240

QY 241 ALHIAIERCKHYVELLVQAQADVHAQARGFPQKDEGGYFYGELPLSLAACTNQPHI 300
DB 241 SLHIAIERCKHYVELLVQAQADVHAQARGFPQKDEGGYFYGELPLSLAACTNQPHI 300

QY 301 VNYLTENPHKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKLCARLPDS 360
DB 301 VNYLTENPHKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKLCARLPDS 360
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QY 361 NLEAVLNNDGLSPLMAAATGKIGIFQHIIRREVTDTRHLRSRKFQDWAYGVPVYSSLYD 420
 DB 361 NLEAVLNNDGLSPLMAAATGKIGIFQHIIRREVTDTRHLRSRKFQDWAYGVPVYSSLYD 420
 QY 421 LSSLDTCGEEASVLEILVNSKIENRHEMLAVEPINEILLRDKWRKFGAVSFYINVVSYLC 480
 DB 421 LSSLDTCGEEASVLEILVNSKIENRHEMLAVEPINEILLRDKWRKFGAVSFYINVVSYLC 480
 QY 481 AMVIFTLTAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
 DB 481 AMVIFTLTAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFFFTSIKDLFTKKCPGV 540
 QY 541 NSLFDGSGFQLLYFYISVLVIVSAALYLAGIAYLAVMVFAVLVGMNLYFTTGLKLTG 600
 DB 541 NSLFDGSGFQLLYFYISVLVIVSAALYLAGIAYLAVMVFAVLVGMNLYFTTGLKLTG 600
 QY 601 TYSIMIQILFKDLFRLLVLLFMIGYASALVSLNPNCKNKCNEODTCTVPTYPSC 660
 DB 601 TYSIMIQILFKDLFRLLVLLFMIGYASALVSLNPNCKNKCNEODTCTVPTYPAC 660
 QY 661 RDSEFTFLDLFKLTIGMGDLEMLSSTKYPVFFIILLVYIITFTVLLNMLIALMGE 720
 DB 661 RDSEFTFLDLFKLTIGMGDLEMLSSTKYPVFFIILLVYIITFTVLLNMLIALMGE 720
 QY 721 TVGQVSKESKHIWKLQ 736
 DB 721 TVGQVSKESKHIWKLQ 736

RESULT 9

QY9EQ24 ID Q9EQ24 PRELIMINARY; PRT; 871 AA.
 AC Q9EQ24; DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE Ion channel.
 GN Name=Trpv4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22692536; PubMed=12692122; DOI=10.1074/jbc.M302561200;
 RT "Impaired pressure sensation in mice lacking TRPV4."
 RL J. Biol. Chem. 278:22664-22668 (2003).
 DR EMBL; AB021875; BAA83731.2; -.
 DR MGD; MGI:1926945; Trpv4.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0005262; F:calcium channel activity; IDA.
 DR GO; GO:0005034; F:osmosensor activity; IDA.
 DR GO; GO:0042538; P:hyperosmotic salinity response; IMP.
 DR GO; GO:0007231; P:osmosensory signaling pathway; IDA.
 DR GO; GO:0047484; P:regulation of response to osmotic stress; IMP.
 DR GO; GO:0030103; P:vasopressin secretion; IMP.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002111; Cat channel_TrpL.
 DR InterPro; IPR005821; Ion trans.
 DR InterPro; IPR004729; TRPChannel.
 DR InterPro; IPR008347; Vanil receptor.
 DR InterPro; IPR008348; vanil_receptor2.
 DR Pfam; PF00023; Ank; 3.
 DR Pfam; PF00520; Ion trans; 1.
 DR PRINTS; PR01768; TRPVRECEPTOR.
 DR PRINTS; PR01769; VRL2RECEPTOR.
 DR SMART; SM00248; ANK; 3.
 DR TIGRFAMs; TIGR00870; trp; 1.
 DR PROSITE; PS50088; ANK REPEAT; 1.
 DR PROSITE; PS50297; ANK REP REGION; 1.
 KW ANK repeat; Ion transport; Ionic channel; Transmembrane; Transport.

SQ SEQUENCE 871 AA; 98060 MW; 3285AE576D32DD95 CRC64;
 Query Match 95.4%; Score 3681; DB 2; Length 871;
 Best Local Similarity 95.2%; Pred. No. 2.7e-222;
 Matches 701; Conservative 17; Mismatches 18; Indels 0; Gaps 0;
 QY 1 MADSEGPRAQGEVAELPGDESGTPGGEAPPLSSLANLFEGEDGSLSPSPADARRPAGP 60
 DB 1 MADPDGPRAAAPGEVAEPGDESGTSGGEAPPLSSLANLFEGEESGSLSPVDASRRPAGP 60
 QY 61 GDGRPNLRMKFQGAFRKGVNPNIDLLSTLTVSSVPGPKAPMDSLFDYGYRHHSDN 120
 DB 61 GDGRPNLRMKFQGAFRKGVNPNIDLLSTLTVSSVPGPKAPMDSLFDYGYRHHSDN 120
 QY 121 KRWRKKIIEKQPSQPKAPAPQPPILKVFNRPIILFDIVSRGSTADLDGLLPLTHKKRL 180
 DB 121 KRWRKVVKEQPSQPKAPAPQPPILKVFNRPIILFDIVSRGSTADLDGLLPLTHKKRL 180
 QY 181 TDESFRPESTGKTCCLPKALLNSGRNDTIPVLDIAERTGNMREFINSPFRDIYRGQT 240
 DB 181 TDESFRPESTGKTCCLPKALLNSGRNDTIPVLDIAERTGNMREFINSPFRDIYRGQT 240
 QY 241 ALHIAIERRCKHYVELLVQAQADVHAQARGFFQPKDEGGYFYFGEPLSLAACTNQPHI 300
 DB 241 SLHIAIERRCKHYVELLVQAQADVHAQARGFFQPKDEGGYFYFGEPLSLAACTNQPHI 300
 QY 301 VNYLTENPHKKADNRDROSGNTVHLVAIADNTRENTKFTVMYDILLKLCARLPFDS 360
 DB 301 VNYLTENPHKKADNRDROSGNTVHLVAIADNTRENTKFTVMYDILLKLCARLPFDS 360
 QY 361 NLEAVLNNDGLSPLMAAATGKIGIFQHIIRREVTDTRHLRSRKFQDWAYGVPVYSSLYD 420
 DB 361 NLEAVLNNDGLSPLMAAATGKIGIFQHIIRREVTDTRHLRSRKFQDWAYGVPVYSSLYD 420
 QY 421 LSSLDTCGEEASVLEILVNSKIENRHEMLAVEPINEILLRDKWRKFGAVSFYINVVSYLC 480
 DB 421 LSSLDTCGEEASVLEILVNSKIENRHEMLAVEPINEILLRDKWRKFGAVSFYINVVSYLC 480
 QY 481 AMVIFTLTAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
 DB 481 AMVIFTLTAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFFFTSIKDLFTKKCPGV 540
 QY 541 NSLFDGSGFQLLYFYISVLVIVSAALYLAGIAYLAVMVFAVLVGMNLYFTTGLKLTG 600
 DB 541 NSLFDGSGFQLLYFYISVLVIVSAALYLAGIAYLAVMVFAVLVGMNLYFTTGLKLTG 600
 QY 601 TYSIMIQILFKDLFRLLVLLFMIGYASALVSLNPNCKNKCNEODTCTVPTYPSC 660
 DB 601 TYSIMIQILFKDLFRLLVLLFMIGYASALVSLNPNCKNKCNEODTCTVPTYPAC 660
 QY 661 RDSEFTFLDLFKLTIGMGDLEMLSSTKYPVFFIILLVYIITFTVLLNMLIALMGE 720
 DB 661 RDSEFTFLDLFKLTIGMGDLEMLSSAKYPVFFIILLVYIITFTVLLNMLIALMGE 720
 QY 721 TVGQVSKESKHIWKLQ 736
 DB 721 TVGQVSKESKHIWKLQ 736
 RESULT 10
 QY9ER27 ID Q9ER27 PRELIMINARY; PRT; 873 AA.
 AC Q9ER27; DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Vanilloid receptor-related osmotically activated channel.
 GN Name=Trpv4; Synonyms=Vroac;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]


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SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus;
RX MEDLINE=20531888; PubMed=11081638; DOI=10.1016/S0092-8674(00)00143-4;
RA Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,
RT Sali A., Hudepeth A.J., Friedman J.M., Heller S.;
RT "vanilloid receptor-related osmotically activated channel (VR-OAC), a
RT candidate vertebrate osmoreceptor.";
RL Cell 103:525-535(2000).
DR EMBL, AF263522; AAG28028.1; -.
DR MGD; MGI:1926945; Trpv4.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005262; F:calcium channel activity; IDA.
DR GO; GO:0005034; F:osmosensor activity; IDA.
DR GO; GO:0042538; P:hyperosmotic salinity response; IMP.
DR GO; GO:0007231; P:osmosensory signaling pathway; IDA.
DR GO; GO:0047484; P:regulation of response to osmotic stress; IMP.
DR GO; GO:0030103; P:vasopressin secretion; IMP.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR004729; TRPChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR InterPro; IPR008348; Vanil_receptor2.
DR Pfam; PF00023; Ank; 3.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR01768; TRPVRECEPTOR.
DR PRINTS; PR01769; VRL2RECEPTOR.
DR SMART; SM00248; ANK; 3.
DR TIGRFAMS; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW Transport.
SQ SEQUENCE 873 AA; 98596 MW; 5DD987C92712B24EA CRC64;

Query Match 94.2%; Score 3636; DB 2; Length 873;
Best Local Similarity 94.4%; Pred. No. 1.8e-219;
Matches 697; Conservative 17; Mismatches 22; Indels 2; Gaps 2;

QY 1 MADSEGRAGGEVAELPGDESGTGGEGAPPLSSLANLFGEDGSLGSPSPA-DASRPAG 59
DB 1 MADPGGPRAAPGEVAEPGDESGTGGEGAPPLSSLANLFGEGESSYFSPRWATASRPAG 60
QY 60 PDGGRPNLRMKF-QGAFKRGVNPIDLLESTLYESSVVGPKAPMDSLFDYGYTRHSS 118
DB 61 PDGGRPNLRMKFGRSAFKRGVNPIDLLESTLYESSVVGPKAPMDSLFDYGYTRHSS 120
QY 119 DNKRWRKXIIKQSPKAPAPQPPPIKLVNRPILFDIVSRGSTADLDGLLPLTHKK 178
DB 121 DNKRWRKXVKEQSPKAPAPQPPPIKLVNRPILFDIVSRGSTADLDGLLPLTHKK 180
QY 179 RLTDSEFPSTGKTCPLKALLNLSNGRNDIPVLDDIAERTGNRREFINPFRDIYVRG 238
DB 181 RLTDSEFPSTGKTCPLKALLNLSNGRNDIPVLDDIAERTGNRREFINPFRDIYVRG 240
QY 239 QTAHLIAIERCKHVVELLVAAQADVHAQAGRFQPKDEGYFYFGLPLSLAACTNOP 298
DB 241 QTSLLIAIERCKHVVELLVAAQADVHAQAGRFQPKDEGYFYFGLPLSLAACTNOP 300
QY 299 HINVTLENPHKKADMRQDSRGNTVLHALVAIAADNTRENTKFTVMYDLLLLKCARLFP 358
DB 301 HINVTLENPHKKADMRQDSRGNTVLHALVAIAADNTRENTKFTVMYDLLLLKCARLFP 360
QY 359 DSNLEAVLNNDGLSLPMAAKTKIGIQHILIRREVTDETRHLSRKFKWAYGVPYSSL 418
DB 361 DSNLEAVLNNDGLSLPMAAKTKIGIQHILIRREVTDETRHLSRKFKWAYGVPYSSL 420
QY 419 YDLSLSDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSY 478
DB 421 YDLSLSDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSY 480
QY 479 LCAMVIFLTATAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFPTTNIKDLFMKKCP 538

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Db 481 LCAMVIFLTATAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFPTTNIKDLFMKKCP 540
QY 539 GWSNLFIDGSGFOLLYFYISVLVIVSAALYLAGIEAYLAWVPALVGLWVNALYFTRGLKL 598
DB 541 GWSNLFIDGSGFOLLYFYISVLVIVSAALYLAGIEAYLAWVPALVGLWVNALYFTRGLKL 600
QY 599 TGTYSIMIOKILFKDLFRFLVYLFLMTGYASALVSLNPNCANMKVCNEDQNTCTVPTYP 658
DB 601 TGTYSIMIOKILFKDLFRFLVYLFLMTGYASALVSLNPNCANMKVCNEDQNTCTVPTYP 660
QY 659 SCRDSESTFLDLFKLTIGWGLEMLSSPKYVWVFILLVYLLFVLLNMLIALM 718
DB 661 ACRDSESTFALLDLFKLTIGWGLEMLSSAKYPVVFILLVYLLFVLLNMLIALM 720
QY 719 GETVQVSKESKHIWKLQ 736
DB 721 GETVQVSKESKHIWKLQ 738

RESULT 11
QY Q96RS7 PRELIMINARY; PRT; 803 AA.
AC Q96RS7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Vanilloid receptor-like protein 2.
GN Name=VRL2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Derst C., Schafer M.K.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF279673; AAK69487.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR004729; TRPChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR InterPro; IPR008348; Vanil_receptor2.
DR Pfam; PF00023; Ank; 3.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR01768; TRPVRECEPTOR.
DR PRINTS; PR01769; VRL2RECEPTOR.
DR SMART; SM00248; ANK; 3.
DR TIGRFAMS; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW Transport.
SQ SEQUENCE 803 AA; 91635 MW; AB329C595B325784 CRC64;

Query Match 90.0%; Score 3472; DB 2; Length 803;
Best Local Similarity 100.0%; Pred. No. 3.1e-209;
Matches 668; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 MKFQGAFRKGVNPIDLLESTLYESSVVGPKAPMDSLFDYGYTRHSSDNKWRKKII 128
DB 1 MKFQGAFRKGVNPIDLLESTLYESSVVGPKAPMDSLFDYGYTRHSSDNKWRKKII 60
QY 129 EKQPSKAPAPQPPPIKLVNRPILFDIVSRGSTADLDGLLPLTHKKRLTDEEFREP 188
DB 61 EKQPSKAPAPQPPPIKLVNRPILFDIVSRGSTADLDGLLPLTHKKRLTDEEFREP 120

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QY 189 STGKTCCLKALLNLSNGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGOTALHIAIER 248
Db 121 STGKTCCLKALLNLSNGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGOTALHIAIER 180
QY 249 RCKHYVELLVAQADVHAQARGFPQKDEGGYFYGELPLSLAECTNPHIVNLTENP 308
Db 181 RCKHYVELLVAQADVHAQARGFPQKDEGGYFYGELPLSLAECTNPHIVNLTENP 240
QY 309 HKKADMRQDSRGNTVLAHALVAIAADNTRENTKFTVMYDMLLKCARLFPDSNLEAVLNN 368
Db 241 HKKADMRQDSRGNTVLAHALVAIAADNTRENTKFTVMYDMLLKCARLFPDSNLEAVLNN 300
QY 369 DGLSPLMAAATGKIGIFQHIIRREVTDETRHLSRKPKOWAYGPVYSSLDLSDTCG 428
Db 301 DGLSPLMAAATGKIGIFQHIIRREVTDETRHLSRKPKOWAYGPVYSSLDLSDTCG 360
QY 429 EEASVLEILVNSKTIENHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLCAMVIFTLT 488
Db 361 EEASVLEILVNSKTIENHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLCAMVIFTLT 420
QY 489 AYYQLEGTPPYPRYRTVDYLRAGEVITLFTGVLFFFFTNFKDLPMKCPGVNSLFDGS 548
Db 421 AYYQLEGTPPYPRYRTVDYLRAGEVITLFTGVLFFFFTNFKDLPMKCPGVNSLFDGS 480
QY 549 FOLLFYISVLVISAALYLAGIEAYLAVMVPALVGLMNNALYFTRGLKLTGTYSIMIOK 608
Db 481 FOLLFYISVLVISAALYLAGIEAYLAVMVPALVGLMNNALYFTRGLKLTGTYSIMIOK 540
QY 609 ILFKDLFRLLVYLLFMIGYASALVSLNPNCAVMKVCNEDQTNCTVPTPSCRDETEST 668
Db 541 ILFKDLFRLLVYLLFMIGYASALVSLNPNCAVMKVCNEDQTNCTVPTPSCRDETEST 600
QY 669 FLDDLFLKLTIGMDLEMLSSTKYPVVFVILLVYIILTFVLLNMLIALMGETVGVQSK 728
Db 601 FLDDLFLKLTIGMDLEMLSSTKYPVVFVILLVYIILTFVLLNMLIALMGETVGVQSK 660
QY 729 SKHIWKLQ 736
Db 661 SKHIWKLQ 668
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RESULT 12

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Q8NG64
ID Q8NG64 PRELIMINARY; PRT; 811 AA.
AC Q8NG64;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE OTRPCbeta cation channel.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aortic endothelium;
RA Xu P., Satoh E., Iijima T.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB073669; BAC06573.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; P:cation channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR008347; Vanil_receptor.
DR InterPro; IPR008348; Vanil_receptor2.
DR Pfam; PF00023; Ank; 3.
DR Pfam; PF00520; Ion trans; 1.
DR PRINTS; PR01415; ANKTRIN.
DR PRINTS; PR01768; TRPVECEPTOR.
DR PRINTS; PR01769; VRL2RECEPTOR.
DR SMART; SM00248; ANK; 3.
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DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT; 1.
KW ANK repeat; Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 811 AA; 91220 MW; 3847D0FD07830781 CRC64;

Query Match 89.8%; Score 3466; DB 2; Length 811;
Best Local Similarity 91.6%; Pred. No. 7.5e-209;
Matches 674; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 MADSEGPRAAGPGEVAELPGDESGTPEGAEAPPLSLANLFEGEDGSLSPSPADASRPAGP 60
Db 1 MADSEGPRAAGPGEVAELPGDESGTPEGAEAPPLSLANLFEGEDGSLSPSPADASRPAGP 60
QY 61 GDGPNLRMKFQGAAPRGVNPPIIDLESTLYESSVVPKAPMDSLFDYGYRHHSSDN 120
Db 61 GDGPNLRMKFQGAAPRGVNPPIIDLESTLYESSVVPKAPMDSLFDYGYRHHSSDN 120
QY 121 KRWKKIIEKQPSKPAPAPQPPILKVFNRPIIPDIIVSRGSTADLDGLLPLLLTHKKRL 180
Db 121 KRWKKIIEKQPSKPAPAPQPPILKVFNRPIIPDIIVSRGSTADLDGLLPLLLTHKKRL 180
QY 181 TDEFRPESTCKTCLPKALLNLSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGOT 240
Db 181 TDEFRPESTCKTCLPKALLNLSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGOT 240
QY 241 ALHIAIERRCKHYVELLVAQADVHAQARGFPQKDEGGYFYGELPLSLAECTNPHI 300
Db 241 ALHIAIERRCKHYVELLVAQADVHAQARGFPQKDEGGYFYGELPLSLAECTNPHI 300
QY 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIAADNTRENTKFTVMYDMLLKCARLFPDS 360
Db 301 VNYLTENPHKADMRQDSRGNTVLAHALVAIAADNTRENTKFTVMYDMLLKCARLFPDS 360
QY 361 NLEAVLNNDGSLPLMAAATGKIGIFQHIIRREVTDETRHLSRKFKDWAYGPVYSSLYD 420
Db 361 NLEAVLNNDGSLPLMAAATGKIGIFQHIIRREVTDETRHLSRKFKDWAYGPVYSSLYD 420
QY 421 LSLDTCGEASVLEILVNSKIENHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
Db 385 -----NRHEMLAAEPINELLRDKWRKFGAVSFYINVVSYLC 420
QY 481 AMVIFTLTAYQPLEGTPPYPRYRTVDYLRAGEVITLFTGVLPFFFTNFKDLPMKCPGV 540
Db 421 AMVIFTLTAYQPLEGTPPYPRYRTVDYLRAGEVITLFTGVLPFFFTNFKDLPMKCPGV 480
QY 541 NSLFDGSGFOLLFYISVLVISAALYLAGIEAYLAVMVPALVGLMNNALYFTRGLKLTG 600
Db 481 NSLFDGSGFOLLFYISVLVISAALYLAGIEAYLAVMVPALVGLMNNALYFTRGLKLTG 540
QY 601 TYSIMIQILFKDLFRLLVYLLFMIGYASALVSLNPNCAVMKVCNEDQTNCTVPTPSC 660
Db 541 TYSIMIQILFKDLFRLLVYLLFMIGYASALVSLNPNCAVMKVCNEDQTNCTVPTPSC 600
QY 661 RDETFSTFLDLPLKLTIGMDLEMLSSTKYPVVFVILLVYIILTFVLLNMLIALMGE 720
Db 601 RDETFSTFLDLPLKLTIGMDLEMLSSTKYPVVFVILLVYIILTFVLLNMLIALMGE 660
QY 721 TVGVQSKESKHIWKLQ 736
Db 661 TVGVQSKESKHIWKLQ 676

RESULT 13
Q91XR5
ID Q91XR5 PRELIMINARY; PRT; 803 AA.
AC Q91XR5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Vanilloid receptor-like protein 2.
GN Name=trpv4; Synonyms=Vrl2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Kidney;
RC Derst C., Schafer M.K.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF279672; AAK69486.1; -
DR MGD; MGI:1326945; Trp4.
DR GO; GO:0016021; C:integral to membrane, TAS.
DR GO; GO:0005262; F:calcium channel activity; IDA.
DR GO; GO:0005034; F:osmosensor activity; IDA.
DR GO; GO:0042538; P:hyperosmotic salinity response; IMP.
DR GO; GO:0007231; P:osmosensory signaling pathway; IDA.
DR GO; GO:0047484; P:regulation of response to osmotic stress; IMP.
DR GO; GO:0030103; P:vasopressin secretion; IMP.
DR Pfam; PF00023; Ank; 3.
DR PROSITE; PS00520; Ion trans; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR01768; TRPVRECEPTOR.
DR PRINTS; PR01769; VRL2RECEPTOR.
DR SMART; SM00248; Ank; 3.
DR TIGRFAMs; TIGR00870; trp; 1.
DR PROSITE; PS00088; ANK REPEAT; 1.
DR PROSITE; PS0297; ANK REP REGION; 1.
DR ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW Transport.
SQ SEQUENCE. 803 AA; 91438 MW; 79A5B9233300029 CRC64;

Query Match 87.8%; Score 3389; DB 2; Length 803;
Best Local Similarity 96.6%; Pred. No. 5e-204;
Matches 645; Conservative 14; Mismatches 9; Indels 0; Gaps 0;
QY 69 MKFOAFKGVNPNIDLLSTLYESVVPKPKAPMDSLFYGYTRHSSDNKRKKII 128
DB 1 MKFOAFKGVNPNIDLLSTLYESVVPKPKAPMDSLFYGYTRHSSDNKRKKVV 60
QY 129 EKQPSKPAPQPPPIKVFNRPIFDIVSRGSTADLDGLLPFLTHKKRLTDEEFP 188
DB 61 EKQPSKPAPQPPPIKVFNRPIFDIVSRGSTADLDGLLSFLTHKKRLTDEEFP 120
QY 189 STGKTCPLKALNLSNGRNDITPVLDDAERTGNMREFINSFPRDIYRGOTLHAIER 248
DB 121 STGKTCPLKALNLSNGRNDITPVLDDAERTGNMREFINSFPRDIYRGOTLHAIER 180
QY 249 RCKHYVELLVAGQADVHAQARGFPQPKDEGGYFYGELPLSLAACTNQHIVNLTENP 308
DB 181 RCKHYVELLVAGQADVHAQARGFPQPKDEGGYFYGELPLSLAACTNQHIVNLTENP 240
QY 309 HKKADMRQDSRGNTVLHALVAIAADNTRENTKFTKMDYDILLKCARLPDPSNLEAVLNN 368
DB 241 HKKADMRQDSRGNTVLHALVAIAADNTRENTKFTKMDYDILLKCARLPDPSNLEAVLNN 300
QY 369 DGLSPLMAAATGKIGFQHIIRREVTDETHLSRKPKDWAYGVPVSSLYDLSLDTG 428
DB 301 DGLSPLMAAATGKIGFQHIIRREVTDETHLSRKPKDWAYGVPVSSLYDLSLDTG 360
QY 429 EEASVLEILVNSKLENHMLAVEPINELLARDKWRKFGAVSYINVSYLCAVMIFFLT 488
DB 361 EEASVLEILVNSKLENHMLAVEPINELLARDKWRKFGAVSYINVSYLCAVMIFFLT 420
QY 489 AYYQLEGTPPYRTTVDYLRAGEVITLFTGVLFVFFFTNKDLFMKCKPGVNSLFDGS 548
DB 421 AYYQLEGTPPYRTTVDYLRAGEVITLFTGVLFVFFFTNKDLFMKCKPGVNSLFDGS 480
QY 549 FOLLYFIYSVLVISAALYLAGIEAYLAAMVFAVVLGWMNALYFTRGLKLTGTYSIMIQ 608
DB 481 FOLLYFIYSVLVISAALYLAGIEAYLAAMVFAVVLGWMNALYFTRGLKLTGTYSIMIQ 540
QY 609 ILFKDLFFFLAVLLFMIGYASALVSLANPCANMKVCNEDOTNCTVTPYPSCRDSEFT 668
DB 541 ILFKDLFFFLAVLLFMIGYASALVSLANPCANMKVCNEDOTNCTVTPYPSCRDSEFT 600

QY 669 FLDDLFLKLTIGMGDLEMLSSKYPVVFILLVYIILTFVLLNMLIALMGSTVQVSKE 728
DB 601 FLDDLFLKLTIGMGDLEMLSSKYPVVFILLVYIILTFVLLNMLIALMGSTVQVSKE 660
QY 729 SKHIWKLQ 736
DB 661 SKHIWKLQ 668
RESULT 14
Q9DFS3
ID Q9DFS3 PRELIMINARY; PRT; 852 AA.
AC Q9DFS3;
DT 01-WAR-2001 (TRENBLrel. 16, Created)
DT 01-WAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-WAR-2004 (TRENBLrel. 26, Last annotation update)
DE Vanilloid receptor-related osmotically activated channel protein.
GN Name=VR-OAC;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP SEQUENCE FROM N.A.
RC TISSUE=Cochlea;
RX MEDLINE=20531888; PubMed=11081638; DOI=10.1016/S0092-8674(00)00143-4;
RA Liedtke W., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S., Sali A.,
RA Hudspeth A.J., Friedman J.M., Heller S.;
RT "Vanilloid receptor-related osmotically activated channel (VR-OAC), a
RT candidate vertebrate osmoreceptor.";
RL Cell 103:525-535(2000).
DR EMBL; AF261883; AAG28026.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR002016; Peroxidase.
DR InterPro; IPR001865; Ribosomal S2.
DR InterPro; IPR004729; TrpChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR InterPro; IPR008348; Vanil_receptor2.
DR Pfam; PF00023; Ank; 3.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR01768; TRPVRECEPTOR.
DR PRINTS; PR01769; VRL2RECEPTOR.
DR SMART; SM00248; Ank; 3.
DR TIGRFAMs; TIGR00870; trp; 1.
DR PROSITE; PS00088; ANK REPEAT; 1.
DR PROSITE; PS0297; ANK REP REGION; 1.
DR PROSITE; PS00436; PEROXIDASE 2; UNKNOWN 1.
DR PROSITE; PS00962; RIBOSOMAL S2 1; UNKNOWN 1.
KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW Transport.
SQ SEQUENCE. 852 AA; 96197 MW; E85365D3FADD08C1 CRC64;
Query Match 85.1%; Score 3284; DB 2; Length 852;
Best Local Similarity 86.5%; Pred. No. 2.1e-197;
Matches 624; Conservative 43; Mismatches 50; Indels 4; Gaps 2;
QY 17 ELPDSEGTGPGGAFLSSLANLFEGDGLSPSPADSR-PAGPGDPRNLRMKFGAF 75
DB 5 EDPDAGDVLGDGDSFPLSSLANLFVEVD--TFSPAEPGRGPGAGDGKQLRMKFGAF 61
QY 76 RKGVPNPDIDLESTLYESSVVPKPKAPMDSLFYGYTRHSSDNKRKKIIIEKQPS 135
DB 62 RKGPKWELLESTLYESSVVPKPKAPMDSLFYGYTRHSSDNKRKKIIEKQPS 121
QY 136 KAPAPQPPPIKVFNRPIFDIVSRGSTADLDGLLPFLTHKKRLTDEEFPSTGKTC 195

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Db 122 KGPAENPPVLRNRPVLFIDVSRGSDGLEGLSFLTHKKRLTDEFEPRSTGKTC 181
Qy 196 PKALLNLNGRNDTTPVLLDIAERTGNMREFINSFPRDIYRGQATALHAIERRCKHYVE 255
Db 182 PKALLNLNGRNDTTPVLLDIAERTGNMREFINSFPRDIYRGQATALHAIERRCKHYVE 241
Qy 256 LLVAGQADVHAQARGFRFPQKDEGGYFYFGEPLSLAACTNQPHIVNYLTENPHKKADMR 315
Db 242 LLVKGADVHAQARGFRFPQKDEGGYFYFGEPLSLAACTNQPHIVNYLTENPHKKADMR 301
Qy 316 RODSGNTVLHALVAIAONTRENTKFTVMYDOLLKCARLPDPSNLEAVLNDGLSPIM 375
Db 302 RODSGNTVLHALVAIAONTRENTKFTVMYDOLLKCARLPDPSNLEAVLNDGLSPIM 361
Qy 376 MAAKTKGIGIFOHIIIRREVTDETRHLSRKFKDMAYGPVYSSLYDLSSIDTCGEASVLE 435
Db 362 MAAKTKGIGIFOHIIIRREIADVEDRHLRSKFKDMAYGPVYSSLYDLSSIDTCGEASVLE 421
Qy 436 ILVNSKIENRHEMLAVEPINELLRDWRKFGAVSYINVSYLCAWVIFTLTAYYQPLE 495
Db 422 ILVNSKIENRHEMLAVEPINELLRDWRKFGAVSYINVSYLCAWVIFTLTAYYQPLE 481
Qy 496 GTPPPYPTTVDYLRAGEVITLFCVLFFFTNIKDLFMKKCPGNSLFDGSGFOLLIFYI 555
Db 482 GTPPPYPTTVDYLRAGEVITLFCVLFFFTNIKDLFMKKCPGNSLFDGSGFOLLIFYI 541
Qy 556 YSVLVISAAALYAGIEAYLAVMVFALVGMNVALYFTRGLKLTCTYSIMIQILFKDLF 615
Db 542 YSVLVISAAALYAGIEAYLAVMVFALVGMNVALYFTRGLKLTCTYSIMIQILFKDLF 601
Qy 616 RFLVLLFMIGYASALVSLNPNCAVMKVCNBDQNTCTVPTYPSCRDSETFTFLDLFK 675
Db 602 RFLVLLFMIGYASALVSLNPNCAVMKVCNBDQNTCTVPTYPSCRDSETFTFLDLFK 661
Qy 676 LTIGMGDLEMSSTKYPPVFIILLVYIILTPVLLNLMLALMGTVGVQVSKESKHIWKL 735
Db 662 LTIGMGDLEMSSTKYPPVFIILLVYIILTPVLLNLMLALMGTVGVQVSKESKHIWKL 721
Qy 736 Q 736
Db 722 Q 722

RESULT 15
Q8QFN9 PRELIMINARY; PRT; 843 AA.
AC Q8QFN9;
DC Q8QFN9;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Vanilloid receptor-like protein.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Dorsal root ganglia;
RX MEDLINE=21842900; PubMed=11853675; DOI=10.1016/S0092-8674(02)00637-2;
RA Jordt S.E., Julius D.;
RT "Molecular basis for species-specific sensitivity to 'hot' chili
RT peppers.";
RL Cell 108:421-430(2002).
DR EMBL; AY072909; AAL78069.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
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DR InterPro; IPR004729; TRPChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR InterPro; IPR008348; Vanil_receptor2.
DR Pfam; PF00023; Ank; 3.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR01415; ANKTRIN.
DR PRINTS; PR01768; TRPVRECEPTOR.
DR PRINTS; PR01769; VRL2RECEPTOR.
DR SMART; SMO0248; ANK; 4.
DR TIGRFAMs; TIGR00870; tlp; 1.
DR PROSITE; PS00088; ANK_REPEAT; 1.
DR PROSITE; PS02997; ANK_REPEAT_REGION; 1.
KW ANK repeat; Ion channel; Receptor; Transmembrane;
KW Transport.
SQ SEQUENCE 843 AA; 96520 MW; ABB3592C9DC179C8 CRC64;

Query Match 41.6%; Score 1604.5; DB 2; Length 843;
Best Local Similarity 47.5%; Pred.No. 4.7e-92;
Matches 343; Conservative 128; Mismatches 184; Indels 67; Gaps 18;

Qy 41 EGEDGSLSPSPADASRPAGDGRPNLRMKFGAFKGVNPNIDLLESTLY--ESSVVRG 98
Db 27 DGEDSAL--ETAD-----NLOGT-----SNKVQPSKSNIPARRGRFVWG 64

Qy 99 ---PKKAPMDSLEFY-----GTVRHSSDNKRWRKIIIEKQP---QSPKAPAPQPPPL 146
Db 65 CDCOMAPMDSFYQMDHLMAPSVIKFHAMBERGKHLKLLSTDITGCSSEKA-----F 116

Qy 147 KVFNRPIFLDIVSGSTADLDGLLPFLTHKKRLTDEFRSPSTGKTCCLPKALLNLSGR 206
Db 117 KFYRRIRFDVARGSTKDLDDLILLYLNRTLKHLTDDDFKPEPKETGKTCCLLKAWMLHDK 176

Qy 207 NDTTPVLIDIAERTGNMREFINSFPRDIYRGQATALHAIERRCKHYVELLVAQGDVHA 266
Db 177 NDTPLLLDIAKGTGLKEFNAEYTDNYKQATALHAIERRNNMYLVKLLVQNGADVHA 236

Qy 267 QARGRFPO- KDEGGYFYFGEPLSLAACTNQPHIVNYLTENPHKKADMRDSDRGNTVL 325
Db 237 RACGEFFRKIKGKPG-FYFGEPLSLAACTNQCLIVKELLENPYQAADIAAEDSMGNMVL 295

Qy 326 HALVAIAONTRENTKFTVMYDOLLKCARLPDPSNLEAVLNDGLSLPMLMAAKTGKIGI 385
Db 296 HTLVEIADNTKNTKFTVMYNNILILGAKINPILKBEELTNKKGLTPTLTLAAKTGKIGI 355

Qy 386 FOHIIIRREVTDETRHLSRKFKDMAYGPVYSSLYDLSSIDTCGEASVLEILVYNSKIEN 445
Db 356 FAYILRREIKDPECHLSRKFTEWAYGPHSLSYDLSCIDTC-EKNSVLEIITAYSETN 414

Qy 446 RHEMLAVEPINELLRDWRKFGAVSYINVSYLCAWVIFTLTAYYQPLE--GTPPYPY- 502
Db 415 RHEMLLVEPLNRLQLDKWDRFVGHLYFENFVYATHISILITAAAYRVPQKGDKPPFAR 474

Qy 503 RTVDYLRAGEVITLFCVLFFFTNIKDLFMKKCPGNSLFDGSGFOLLIFYIYSLVIV 562
Db 475 HSTGEYFRTVEILSVLGLYFFFRGIIQ-YFQRRPSLKLTLIVDSYSEVLFVHSLLLLS 533

Qy 563 SAALYLAGIEAYLAVMVFALVGMNVALYFTRGLKLTCTYSIMIQILFKDLFRLLVVL 622
Db 534 SVVLVFCQELVVASWFSALGHWANMLYTRGFQOMGIYSVMIAKMLRDLRCRFMYVL 593

Qy 623 LFMIGYASALVSLNPNCAVMKVCNBDQ-TNCTVPTYPSCRDSETFTST-----FLDLF 674
Db 594 VFLGFSVAVTLIED-----DNEGQDNTSS--EYARCSTKRGRTSYNSLYTCLF 645

Qy 675 KLITGMGDLEMSSTKYPPVFIILLVYIILTPVLLNLMLALMGTVGVQVSKESKHIWKL 734
Db 646 KFTIGMGDLEFTENYRFKSVFILLVLYIILTPVLLNLMLALMGTVGVQVSKESKHIWKL 705

Qy 735 LQ 736
Db 706 LQ 707
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Thu May 5 18:57:48 2005

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Page 12

Search completed: May 4, 2005, 22:12:24
Job time : 89 secs